

Table 1: Genes in the Application

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
1	2	RXA02702	GR00758	1572	115	UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8)
3	4	RXA02705	GR00758	5803	4388	UDP-N-ACETYLMURAMOYLALANINE-D-GLUTAMATE LIGASE (EC 6.3.2.9)
5	6	RXA01254	GR00365	3807	2539	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE (EC 6.3.2.13)
7	8	RXN02707	VV0017	20110	18581	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE--D-ALANYL-D-ALANYL LIGASE
9	10	F RXA02707	GR00758	7264	6920	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE--D-ALANYL-D-ALANYL LIGASE (EC 6.3.2.15)
11	12	F RXA02708	GR00758	7694	7260	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE--D-ALANYL-D-ALANYL LIGASE (EC 6.3.2.15)
13	14	F RXA02709	GR00758	8451	7723	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE--D-ALANYL-D-ALANYL LIGASE (EC 6.3.2.15)
15	16	RXA02710	GR00758	10035	8473	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE (EC 6.3.2.13)
17	18	RXN00531	VV0079	19063	19557	FINE TANGLED PILI MAJOR SUBUNIT
19	20	RXA00944	GR00259	1573	602	NADPH DEHYDROGENASE 3 (EC 1.6.99.1)
21	22	RXS02560	VV0101	9922	10788	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
23	24	RXS03119	VV0098	86877	87008	SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1)
25	26	RXS03120	VV0098	87351	87476	SUPEROXIDE DISMUTASE [MNI] (EC 1.15.1.1)

Cell wall biosynthesis

<u>Nucleic Acid SEQ ID NO</u>	<u>Amino Acid SEQ ID NO</u>	<u>Identification Code</u>	<u>Contig.</u>	<u>NT Start</u>	<u>NT Stop</u>	<u>Function</u>
27	28	RXA01430	GR00417	7458	6271	N-ACETYLMURAMOYL-L-ALANINE AMIDASE (EC 3.5.1.28)
29	30	RXA02641	GR00749	5097	3022	N-ACETYLMURAMOYL-L-ALANINE AMIDASE (EC 3.5.1.28)
31	32	RXA00135	GR00021	1709	2962	UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.7)
33	34	RXA02706	GR00758	6910	5813	PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (EC 2.7.8.13)
35	36	RXA02411	GR00703	1845	997	GLUTAMATE RACEMASE (EC 5.1.1.3)
37	38	RXN01022	VV0143	4460	3381	D-ALANINE--D-ALANINE LIGASE (EC 6.3.2.4)
39	40	F RXA01022	GR00292	3	806	D-ALANINE--D-ALANINE LIGASE (EC 6.3.2.4)
41	42	RXA02703	GR00758	2698	1610	UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE) PYROPHOSPHORYL- UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE (EC 2.4.1.-)
43	44	RXA02711	GR00758	12273	10162	PENICILLIN-BINDING PROTEIN 2

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45	46	RXA02859	GR10005	846	121	PENICILLIN-BINDING PROTEIN 5* PRECURSOR (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE) (EC 3.4.16.4)
47	48	RXA00569	GR00152	3928	4953	PENICILLIN-BINDING PROTEIN 4
49	50	RXN03092	VV0054	10445	9561	PENICILLIN-BINDING PROTEIN 1A
51	52	F RXA00594	GR00158	3525	4457	PENICILLIN-BINDING PROTEIN 1A
53	54	RXA01828	GR00516	7736	6315	PENICILLIN-BINDING PROTEIN 3
55	56	RXA00612	GR00162	3	1187	PENICILLIN-BINDING PROTEIN 1A
57	58	RXA01510	GR00424	15370	16650	PENICILLIN-BINDING PROTEIN 4 PRECURSOR (PBP-4) (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE) (EC 3.4.16.4) / D-ALANYL-D-ALANINE-ENDOPEPTIDASE (EC 3.4.99.-)
59	60	RXN01608	VV0139	3536	5374	PENICILLIN-BINDING PROTEIN 5 PRECURSOR
61	62	F RXA01608	GR00449	837	2675	(AL008883) penicillin binding protein [Mycobacterium tuberculosis]
63	64	RXA01270	GR00367	21652	20498	perosamine synthetase
65	66	RXN00549	VV0079	31746	33419	PENICILLIN-BINDING PROTEIN 1A
67	68	RXN00550	VV0079	33457	33777	PENICILLIN-BINDING PROTEIN 1A
69	70	RXN03091	VV0054	9515	8970	PENICILLIN-BINDING PROTEIN 1A
71	72	RXN03178	VV0334	921	121	PENICILLIN-BINDING PROTEIN 5* PRECURSOR (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE) (EC 3.4.16.4)
73	74	F RXA02859	GR10005	846	121	PENICILLIN-BINDING PROTEIN 5* PRECURSOR (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE) (EC 3.4.16.4)
75	76	RXN01267	VV0009	17895	16582	UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.7)
77	78	RXN00045	VV0119	4409	5317	UDP-N-acetylglucosamine-2-epimerase (EC 5.1.3.14) /N-acetylmannosamine kinase (EC 2.7.1.60)

Cell division

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
79	80	RXN02704	VV0017	16043	14355	CELL DIVISION PROTEIN FTSW
81	82	F RXA02704	GR00758	4382	2694	CELL DIVISION PROTEIN FTSW
83	84	RXA02722	GR00759	2729	1404	CELL DIVISION PROTEIN FTSZ
85	86	RXA00009	GR00002	1545	646	CELL DIVISION PROTEIN FTSX
87	88	RXA00010	GR00002	2248	1562	CELL DIVISION ATP-BINDING PROTEIN FTSE
89	90	RXA00143	GR00022	6328	4847	CELL DIVISION INHIBITOR
91	92	RXA00277	GR00043	1588	5	CELL DIVISION CONTROL PROTEIN 15 (EC 2.7.1.-)
93	94	RXA00857	GR00233	2	1291	CELL DIVISION PROTEIN FTSK
95	96	RXA01435	GR00418	2	871	CELL DIVISION CONTROL PROTEIN 15 (EC 2.7.1.-)
97	98	RXA01511	GR00424	16655	17596	CELL CYCLE PROTEIN MESJ
99	100	RXA01513	GR00424	18368	20926	CELL DIVISION PROTEIN FTSK (EC 3.4.24.-)
101	102	RXA02098	GR00630	4161	5906	CELL DIVISION PROTEIN FTSY
103	104	RXA02713	GR00758	14077	13067	Hypothetical Cell Division Protein mraW
105	106	RXN02723	VV0017	11745	11080	FTSQ
107	108	F RXA02723	GR00759	3460	2984	FTSQ
109	110	RXA01426	GR00417	2777	3403	GLUCOSE INHIBITED DIVISION PROTEIN B

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
111	112	RXA01428	GR00417	4495	5631	STAGE 0 SPORULATION PROTEIN J
113	114	RXA01640	GR00456	4661	1344	STAGE III SPORULATION PROTEIN E
115	116	RXA01829	GR00516	9058	7736	STAGE V SPORULATION PROTEIN E
117	118	RXA01427	GR00417	3512	4432	SOJ PROTEIN
119	120	RXN02973	VV0229	657	4	SOJ PROTEIN
121	122	F RXA01603	GR00447	14043	14663	SOJ PROTEIN
123	124	RXN00818	VV0054	28524	27685	INHIBITION OF MORPHOLOGICAL DIFFERENTIATION

Proteolysis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
125	126	RXN03028	VV0008	41156	43930	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
127	128	F RXA02470	GR00715	2216	3196	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
129	130	F RXA02471	GR00715	3159	4991	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
131	132	RXN03094	VV0057	1794	43	CLPB PROTEIN
133	134	F RXA01668	GR00464	2205	3920	CLPB PROTEIN
135	136	RXN02937	VV0098	85783	85382	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
137	138	RXN03077	VV0043	1729	2913	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
139	140	F RXA02855	GR10002	1693	2877	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14), hippurate hydrolase
141	142	RXN00982	VV0149	7596	6091	(L42758) proteinase [Streptomyces lividans]
143	144	F RXA00977	GR00275	1647	2660	(L42758) proteinase [Streptomyces lividans]
145	146	F RXA00982	GR00276	5194	4949	(L42758) proteinase [Streptomyces lividans]
147	148	RXN01181	VV0065	1	957	AMINOPEPTIDASE AI (EC 3.4.11.1)
149	150	F RXA01181	GR00337	1	957	AMINOPEPTIDASE
151	152	RXN01014	VV0209	13328	10728	AMINOPEPTIDASE N (EC 3.4.11.2)
153	154	F RXA01014	GR00289	3	1580	AMINOPEPTIDASE N (EC 3.4.11.2)
155	156	F RXA01018	GR00290	2289	3152	AMINOPEPTIDASE N (EC 3.4.11.2)
157	158	RXN01046	VV0015	47863	49641	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
159	160	RXN01974	VV0218	3793	5577	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
161	162	RXN01120	VV0182	5678	4401	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX
163	164	F RXA01120	GR00310	2349	1072	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX
165	166	RXN00397	VV0025	3803	4603	XAA-PRO AMINOPEPTIDASE (EC 3.4.11.9)
167	168	RXN01868	VV0127	9980	11905	ZINC METALLOPROTEASE (EC 3.4.24.-)
169	170	F RXA01868	GR00534	1640	30	ZINC METALLOPROTEASE (EC 3.4.24.-)
171	172	F RXA01869	GR00534	1954	1652	ZINC METALLOPROTEASE (EC 3.4.24.-)
173	174	RXN00499	VV0086	8158	9438	PROLINE IMINOPEPTIDASE (EC 3.4.11.5)
175	176	F RXA00499	GR00125	3	959	PROLINE IMINOPEPTIDASE
177	178	RXN01277	VV0009	32155	34158	PROLYL ENDOPEPTIDASE (EC 3.4.21.26)
179	180	F RXA01277	GR00368	1738	50	PROLYL ENDOPEPTIDASE (EC 3.4.21.26)
181	182	RXN00675	VV0005	33258	34049	METHIONINE AMINOPEPTIDASE (EC 3.4.11.18)
183	184	F RXA00675	GR00178	2	484	METHIONINE AMINOPEPTIDASE (EC 3.4.11.18)
185	186	RXN00877	VV0099	2221	3885	PEPTIDYL-DIPEPTIDASE DCP (EC 3.4.15.5)
187	188	F RXA00877	GR00242	3	1067	PEPTIDYL-DIPEPTIDASE DCP (EC 3.4.15.5)

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189	190	RXN01226	VW0064	4172	4711	PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29)
191	192	RXN01963	VW0200	689	6	Hypothetical Secretory Serine Protease (EC 3.4.21.-)
193	194	RXN00621	VW0135	5853	5071	PROTEASE II (EC 3.4.21.83)
195	196	F RXA00621	GR00163	4075	4857	PTRB periplasmic protease
197	198	RXN00622	VW0135	5150	3735	PROTEASE II (EC 3.4.21.83)
199	200	F RXA00622	GR00163	4778	6193	PTRB periplasmic protease
201	202	RXN02146	VW0300	14742	15388	PROTEIN P60 PRECURSOR
203	204	RXN03133	VW0127	39393	40076	HYDROGENASE 1 MATURATION PROTEASE (EC 3.4.-.-)
205	206	RXN02820	VW0131	4799	6109	GAMMA-GLUTAMYLTRANSPEPTIDASE (EC 2.3.2.2)
207	208	F RXA02820	GR00801	1	507	GAMMA-GLUTAMYLTRANSPEPTIDASE (EC 2.3.2.2)
209	210	F RXA02000	GR00589	3430	3933	GAMMA-GLUTAMYLTRANSPEPTIDASE (EC 2.3.2.2)
211	212	RXN02944	VW0169	12751	12074	GAMMA-GLUTAMYLTRANSPEPTIDASE (EC 2.3.2.2)
213	214	RXS00197	VW0115	2733	1522	Membrane Spanning Protease
215	216	RXS01223	VW0064	7528	8139	PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29)
217	218	RXS01642	VW0005	49423	48182	Serine protease

Enzymes in general

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219	220	RXA01728	GR00489	2452	1478	BETA C-S LYASE (EC 3.-.-.-) PUTATIVE AMINOTRANSFERASE
221	222	RXA02214	GR00650	954	1562	Acetyltransferases
223	224	RXA02716	GR00758	16827	17387	Acetyltransferases
225	226	RXN01499	VW0008	7034	3213	ENTEROBACTIN SYNTHETASE COMPONENT F
227	228	FRXA01499	GR00424	7034	3213	Acetyltransferases (the isoleucine patch superfamily)
229	230	RXN00787	VW0321	3736	5637	D-AMINO ACID DEHYDROGENASE LARGE SUBUNIT (EC 1.4.99.1)
231	232	F RXA00787	GR00209	598	5	D-AMINO ACID DEHYDROGENASE LARGE SUBUNIT (EC 1.4.99.1)
233	234	F RXA00791	GR00210	831	4	D-AMINO ACID DEHYDROGENASE LARGE SUBUNIT (EC 1.4.99.1)
235	236	RXA01057	GR00296	7548	6046	D-AMINO ACID DEHYDROGENASE LARGE SUBUNIT (EC 1.4.99.1)
237	238	RXA01055	GR00296	4821	4720	D-AMINO ACID DEHYDROGENASE SMALL SUBUNIT (EC 1.4.99.1)
239	240	RXA01056	GR00296	5952	5053	D-AMINO ACID DEHYDROGENASE SMALL SUBUNIT (EC 1.4.99.1)
241	242	RXN02021	VW0160	2008	1061	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase (EC 2.3.1.117)
243	244	RXS00949				quinolate dehydrogenase (pyrroloquinoline-quinone) (EC 1.1.99.25)
245	246	RXS00004	VW0196	6930	6460	NITRILASE REGULATOR
247	248	RXS00166	VW0232	3650	4309	Methyltransferase
249	250	RXS00288	VW0079	14586	15596	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
251	252	RXS01114	VW0182	9118	10341	3-KETOACYL-COA THIOLEASE (EC 2.3.1.16)
253	254	RXS01205	VW0268	893	363	UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
255	256	RXS01269	VW0009	21430	20990	UNDECAPRENYL-PHOSPHATE GALACTOSEPHOSPHOTRANSFERASE (EC 2.7.8.6)
257	258	RXS01421	VW0122	16024	15638	ACYLTRANSFERASE (EC 2.3.1.-)
259	260	RXS01491	VW0139	36800	37450	DNA FOR L-PROLINE 3-HYDROXYLASE, COMPLETE CDS
261	262	RXS01572	VW0009	43945	44436	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)

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263	264	RXS02453	WV0107	7370	8122	ACETOIN(DIACETYL) REDUCTASE (EC 1.1.1.5)
265	266	RXS02474	WV0008	47021	46248	(S,S)-butane-2,3-diol dehydrogenase (EC 1.1.1.76)
267	268	RXS02485	WV0007	2359	3459	UDP-N-ACETYLENOLPYRUVYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158)
269	270	RXS02539	WV0057	17332	15815	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
271	272	RXS02578	WV0098	7668	6565	ACYLTRANSFERASE
273	274	RXS02741	WV0074	5768	6733	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
275	276	RXS03061	WV0034	108	437	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
277	278	RXS03150	WV0155	10678	10055	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
279	280	RXS02554				Oxidoreductase (EC 1.1.1.-)
281	282	RXS03058				METHYLTRANSFERASE (EC 2.1.1.-)
283	284	RXS03218				CAFFEYL-COA O-METHYLTRANSFERASE (EC 2.1.1.104)
285	286	F RXA01918	GR00549	4644	5057	CAFFEYL-COA O-METHYLTRANSFERASE (EC 2.1.1.104)
287	288	RXC00110	WV0054	27517	26969	Protein involved in hydrolysis of epoxides
289	290	RXC01971	WV0105	4545	3715	Metal-Dependent Hydrolase

Genes encoding enzymes for the metabolism of inorganic compounds

Phosphate and Phosphonate metabolism

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291	292	RXA02118	GR00636	2124	1783	PHNA PROTEIN
293	294	RXA00078	GR00012	6375	5962	PHNB PROTEIN
295	296	RXA02105	GR00632	294	4	PHNB PROTEIN
297	298	RXN00663	WV0142	10120	11493	PHOH PROTEIN HOMOLOG
299	300	F RXA00663	GR00173	1222	227	PHOH PROTEIN HOMOLOG
301	302	RXA00888	GR00242	14325	15341	PHOH PROTEIN HOMOLOG
303	304	RXA01437	GR00418	3932	2550	PHOSPHATE ACETYLTRANSFERASE (EC 2.3.1.8)
305	306	RXN00778	WV0103	18126	19250	PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
307	308	F RXA00778	GR00205	9079	8246	PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
309	310	RXA02497	GR00720	10059	10985	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
311	312	RXA01477	GR00422	8469	10016	ALKALINE PHOSPHATASE D PRECURSOR (EC 3.1.3.1)
313	314	RXA01509	GR00424	15169	14696	INORGANIC PYROPHOSPHATASE (EC 3.6.1.1)
315	316	RXA00100	GR00014	9512	10111	DEDA PROTEIN, similar to alkaline phosphatase
317	318	RXA00615	GR00162	3355	2774	DEDA PROTEIN
319	320	RXN00250	WV0189	286	1032	DEDA PROTEIN - ALKALINE PHOSPHATASE LIKE PROTEIN
321	322	F RXA02010	GR00602	79	525	DEDA PROTEIN
323	324	RXA02120	GR00636	5021	4260	CARBOXYVINYL-CARBOXYPHOSPHONATE PHOSPHORYLMUTASE (EC 2.7.8.23)
325	326	RXS01000	WV0106	7252	6407	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
327	328	RXS01002	WV0106	8858	8055	PHOSPHONATES TRANSPORT ATP-BINDING PROTEIN PHNC
329	330	RXS01003	WV0106	8055	7252	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
331	332	RXS01902	WV0098	84095	83037	alkaline phosphatase

Fe-Metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
333	334	RXA01967	GR00567	1848	706	FERRIC ENTEROCHELIN ESTERASE HOMOLOG
335	336	RXA00070	GR00011	3436	3867	FERRIC UPTAKE REGULATION PROTEIN
337	338	RXA01934	GR00555	7192	7749	FERRIPYOCHELIN BINDING PROTEIN
339	340	RXN01997	VW0084	33308	33793	FERRITIN
341	342	F RXA01997	GR00586	546	935	FERRITIN
343	344	RXA01082	GR00302	1486	827	IRON REPRESSOR
345	346	RXA01236	GR00358	2185	1241	IRON(III) DICTRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
347	348	RXA01354	GR00393	2692	1757	IRON(III) DICTRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
349	350	RXA01620	GR00451	2585	3532	IRON(III) DICTRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
351	352	RXA02052	GR00624	4586	3795	IRON(III) DICTRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
353	354	RXA00372	GR00078	1653	2729	PERIPLASMIC-IRON-BINDING PROTEIN SHIB
355	356	RXA00088	GR00013	4389	5402	FERRIC ANGUINACTIN-BINDING PROTEIN PRECURSOR
357	358	RXS00156	VW0167	1342	2451	FERROCHELATASE (EC 4.99.1.1)
359	360	RXS00624	VW0135	2018	1332	FERROCHELATASE (EC 4.99.1.1)

Modification and degradation of aromatic compounds

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361	362	RXA00024	GR00003	938	1882	ARYL-ALCOHOL DEHYDROGENASE (NADP+) (EC 1.1.1.91)
363	364	RXA02526	GR00725	4109	5314	3-CARBOXY-CIS-CIS-MUCONATE CYCLOISOMERASE (EC 5.5.1.2)
365	366	RXN02813	VW0128	13120	14118	3-CARBOXY-CIS-CIS-MUCONATE CYCLOISOMERASE HOMOLOG (EC 5.5.1.2)
367	368	F RXA02813	GR00794	651	10	3-CARBOXY-CIS-CIS-MUCONATE CYCLOISOMERASE HOMOLOG (EC 5.5.1.2)
369	370	RXA01113	GR00307	1098	862	4-CARBOXYMUCONOLACTONE DECARBOXYLASE (EC 4.1.1.44)
371	372	RXA02126	GR00637	1556	1876	4-CARBOXYMUCONOLACTONE DECARBOXYLASE (EC 4.1.1.44)
373	374	RXA01465	GR00421	4121	2961	MUCONATE CYCLOISOMERASE (EC 5.5.1.1)
375	376	RXA02316	GR00685	9038	8025	MUCONATE CYCLOISOMERASE (EC 5.5.1.1)
377	378	RXA01464	GR00421	2945	2655	MUCONOLACTONE ISOMERASE (EC 5.3.3.4)
379	380	RXA02603	GR00742	7742	8737	4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-)
381	382	RXN02839	VW0362	3	449	4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-)
383	384	F RXA02839	GR00832	3	419	4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-)
385	386	RXA01502	GR00424	8385	9617	BENZENE 1,2-DIOXYGENASE SYSTEM FERREDOXIN-NAD(+) REDUCTASE COMPONENT (EC 1.18.1.3)
387	388	RXA02828	GR00813	15	572	BIPHENYL-2,3-DIOL 1,2-DIOXYGENASE III (EC 1.13.11.39)
389	390	RXA02064	GR00626	5223	4585	CAFFEYL-COA O-METHYLTRANSFERASE (EC 2.1.1.104)
391	392	RXN00639	VW0128	7858	8712	CATECHOL 1,2-DIOXYGENASE (EC 1.13.11.1)
393	394	F RXA00639	GR00168	665	6	CATECHOL 1,2-DIOXYGENASE (EC 1.13.11.1)
395	396	RXN01653	VW0321	12867	11407	DIBENZOTHIOPHENE DESULFURIZATION ENZYME A
397	398	F RXA00797	GR00212	445	804	DIBENZOTHIOPHENE DESULFURIZATION ENZYME A
399	400	F RXA01653	GR00458	1909	971	DIBENZOTHIOPHENE DESULFURIZATION ENZYME A
401	402	RXN02530	VW0057	5469	6125	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8)
403	404	F RXA02530	GR00726	20	469	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8)
405	406	RXA02083	GR00629	1720	311	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 2 (EC 1.14.13.8)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
407	408	RXA00892	GR00243	2188	1295	PARANITROBENZYL ESTERASE (EC 3.1.1.-)
409	410	RXA02092	GR00629	12153	10516	PARANITROBENZYL ESTERASE (EC 3.1.1.-)
411	412	RXN00658	VW0083	15705	16397	PHENOL 2-MONOXYGENASE (EC 1.14.13.7)
413	414	F RXA00658	GR00170	321	4	PHENOL 2-MONOXYGENASE (EC 1.14.13.7)
415	416	RXA01385	GR00406	5320	3440	PHENOL 2-MONOXYGENASE (EC 1.14.13.7)
417	418	RXN01461	VW0128	12414	13025	PROTocatechuate 3,4-dioxygenase ALPHA CHAIN (EC 1.13.11.3)
419	420	F RXA01461	GR00421	463	5	PROTocatechuate 3,4-dioxygenase ALPHA CHAIN (EC 1.13.11.3)
421	422	RXA01462	GR00421	1167	478	PROTocatechuate 3,4-dioxygenase BETA CHAIN (EC 1.13.11.3)
423	424	RXN00641	VW0128	7440	5950	TOLUATE 1,2-dioxygenase ALPHA SUBUNIT (EC 1.14.12.-)
425	426	F RXA00640	GR00168	1083	1331	TOLUATE 1,2-dioxygenase ALPHA SUBUNIT (EC 1.14.12.-)
427	428	F RXA00641	GR00168	1533	2573	TOLUATE 1,2-dioxygenase ALPHA SUBUNIT (EC 1.14.12.-)
429	430	RXA00642	GR00168	2616	3107	TOLUATE 1,2-dioxygenase ALPHA SUBUNIT (EC 1.14.12.-)
431	432	RXA00643	GR00168	3122	4657	TOLUATE 1,2-dioxygenase BETA SUBUNIT (EC 1.14.12.-)
433	434	RXN01993	VW0182	16	1143	TOLUATE 1,2-dioxygenase ELECTRON TRANSFER COMPONENT
435	436	F RXA01993	GR00584	1	366	VANILLATE DEMETHYLASE (EC 1.14.-)
437	438	F RXA02012	GR00604	2	670	VANILLATE DEMETHYLASE (EC 1.14.-)
439	440	RXA01994	GR00584	373	1347	VANILLATE DEMETHYLASE (EC 1.14.-)
441	442	RXA02535	GR00726	6599	7753	VANILLATE DEMETHYLASE OXIDOREDUCTASE (EC 1.-)
443	444	RXA00964	GR00269	1575	451	XYLENE MONOOXYGENASE ELECTRON TRANSFER COMPONENT
445	446	RXN01466	VW0019	7050	6091	1-hydroxy-2-naphthoate 1,2-dioxygenase (EC 1.13.11.38)
447	448	F RXA01466	GR00422	826	5	ARYLESTERASE (EC 3.1.1.2)
449	450	RXN03036	VW0014	671	6	ARYLESTERASE (EC 3.1.1.2)
451	452	F RXA02895	GR10037	671	6	PROTocatechuate 3,4-dioxygenase BETA CHAIN (EC 1.13.11.3)
453	454	RXA02449	GR00710	1458	2360	CHLOROCATECHOL 1,2-dioxygenase (EC 1.13.11.1)
455	456	RXN00178	VW0174	14670	15554	hydroxyquinol 1,2-dioxygenase (EC 1.13.11.37)
457	458	F RXA00178	GR00028	304	1188	hydroxyquinol 1,2-dioxygenase (EC 1.13.11.37)
459	460	RXA02111	GR00632	4310	5593	HYDROXYQUINOL-1, 2-DIOXYGENASE
461	462	RXA00644				QUINOLINATE SYNTHETASE A
						CIS-1,2-DIHYDROXYCYCLOHEXA-3,5-DIENE-1-CARBOXYLATE
						DEHYDROGENASE (EC 1.3.1.55)
463	464	RXN00177	VW0174	13589	14656	MALEYLACETATE REDUCTASE (EC 1.3.1.32)
465	466	F RXA00177	GR00028	3	290	MALEYLACETATE REDUCTASE (EC 1.3.1.32) metabolism of 2,4,5-trichlorophenoxyacetic acid
467	468	RXA02448	GR00710	340	1428	MALEYLACETATE REDUCTASE (EC 1.3.1.32)
469	470	RXA00048	GR00008	2185	527	3-(3-HYDROXYPHENYL) PROPIONATE HYDROXYLASE
471	472	RXA01126	GR00313	2	565	POSSIBLE 2-HYDROXYHEPTA-2,4-DIENE-1,7- DIOATE ISOMERASE
473	474	RXA01117	GR00309	1713	973	SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (EC 2.8.3.5)
475	476	RXA00772	GR00205	2715	1210	SUCCINYL-COA:COENZYME A TRANSFERASE (EC 2.8.3.-)
477	478	RXA01288	GR00372	2018	1644	SUCCINYL-COA:COENZYME A TRANSFERASE (EC 2.8.3.-)

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvate carboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains." Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," <i>Biochem. Biophys. Res. Commun.</i> , 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," <i>Appl. Microbiol. Biotechnol.</i> , 51(2):223-228 (1999)
AB018530	ftsR		Kimura, E. et al. "Molecular cloning of a novel gene, ftsR, which rescues the detergent sensitivity of a mutant derived from <i>Brevibacterium lactofermentum</i> ," <i>Biosci. Biotechnol. Biochem.</i> , 60(10):1565-1570 (1996)
AB018531	ftsR1; ftsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkl	transketolase	
AB024708	glbB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamoyltransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," <i>Microbiology</i> , 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argK; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transaminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," <i>Mol. Cells</i> , 8(3):286-294 (1998)
AF053071	aroB	Dehydroquininate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," <i>Appl. Environ. Microbiol.</i> , 65(4):1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinase synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete)	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzyme); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in <i>Corynebacterium glutamicum</i> ; Isolation of genes involved in biochemical characterization of corresponding proteins," <i>FEMS Microbiol.</i> , 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol acetyl transferase	
AJ224946	mgo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from <i>Corynebacterium glutamicum</i> ," <i>Eur. J. Biochem.</i> , 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of <i>Corynebacterium glutamicum</i> : The channel is formed by a low molecular mass polypeptide," <i>Biochemistry</i> , 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," <i>Microbiology</i> , 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-threonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Aspartase	Kohama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-tryptophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," <i>J. Bacteriol.</i> , 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," <i>FEMS Microbiol. Lett.</i> , 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," <i>J. Bacteriol.</i> , 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," <i>PNAS USA</i> , 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," <i>FEMS Microbiol. Lett.</i> , 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," <i>J. Microbiol. Biotechnol.</i> , 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," <i>Appl. Environ. Microbiol.</i> , 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxR	Diphtheria toxin repressor	Oguzia, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," <i>J. Bacteriol.</i> , 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," <i>J. Bacteriol.</i> , 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 5S rRNA sequences," <i>J. Bacteriol.</i> , 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," <i>Gene</i> , 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," <i>Gene</i> , 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," <i>J. Gen. Microbiol.</i> , 138:1167-1175 (1992)
M89931	accD; brnQ; yhbW	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbW	Rosol, I. et al. "The Corynebacterium glutamicum accD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," <i>J. Bacteriol.</i> , 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," <i>Arch. Microbiol.</i> , 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," <i>Appl. Environ. Microbiol.</i> , 59(3):791-799 (1993)
U11545	trpD	Anthraniolate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 trpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; cglIIR	Putative type II 5-cytosine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," <i>J. Bacteriol.</i> , 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," <i>Gene</i> , 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?; gamma glutamyl kinase; similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicum proline biosynthetic pathway: A natural bypass of the proA step," <i>J. Bacteriol.</i> , 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of <i>Methylobacillus flagellatum</i> and <i>Corynebacterium glutamicum</i> ," <i>Gene</i> , 175:15-22 (1996)
U35023	thiR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," <i>Arch. Microbiol.</i> , 166(2):76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A <i>Corynebacterium glutamicum</i> gene conferring multidrug resistance in the heterologous host <i>Escherichia coli</i> ," <i>J. Bacteriol.</i> , 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		<i>Corynebacterium glutamicum</i> unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the <i>Brevibacterium lactofermentum</i> tryptophan operon," <i>Nucleic Acids Res.</i> , 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the <i>lysA</i> gene of <i>Corynebacterium glutamicum</i> and possible mechanisms for modulation of its expression," <i>Mol. Gen. Genet.</i> , 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of <i>Corynebacterium glutamicum</i> : Molecular cloning, nucleotide sequence, and expression," <i>Mol. Gen. Genet.</i> , 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," <i>Plant. Mol. Biol.</i> , 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the <i>Corynebacterium glutamicum fda</i> gene: structural comparison of <i>C. glutamicum</i> fructose-1, 6-bisphosphate aldolase to class I and class II aldolases," <i>Mol. Microbiol.</i>
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the <i>dapA</i> gene from <i>Corynebacterium glutamicum</i> ," <i>Nucleic Acids Res.</i> , 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambda corynebophage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," <i>Mol. Microbiol.</i> , 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component I	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," <i>Nucleic Acids Res.</i> , 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," <i>Mol. Microbiol.</i> , 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum, and the attP site of lambda corynebophage," <i>FEMS. Microbiol. Lett.</i> , 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspartate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," <i>Mol. Gen. Genet.</i> , 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomerase," <i>J. Bacteriol.</i> , 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," <i>Mol. Microbiol.</i> , 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," <i>Mol. Microbiol.</i> , 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Psl protein	Jolliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," <i>Mol. Microbiol.</i> , 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," <i>Microbiol.</i> , 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," <i>Mol. Microbiol.</i> , 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," <i>Mol. Microbiol.</i> , 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," <i>Appl. Environ. Microbiol.</i> , 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," <i>J. Bacteriol.</i> , 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," <i>Biochem. Biophys. Res. Commun.</i> , 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," <i>Appl. Microbiol. Biotechnol.</i> , 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," <i>J. Bacteriol.</i> , 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," <i>Antonie Van Leeuwenhoek</i> , 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from <i>Corynebacterium glutamicum</i> ," <i>DNA Seq.</i> , 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from <i>Corynebacterium glutamicum</i> pia-ack operon encoding phosphotransacetylase: sequence analysis," <i>Microbiology</i> , 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera <i>Rhodococcus</i> and <i>Norcardia</i> and evidence for the evolutionary origin of the genus <i>Norcardia</i> from within the radiation of <i>Rhodococcus</i> species," <i>Microbiol.</i> , 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronmeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of <i>Corynebacterium glutamicum</i> ," <i>J. Bacteriol.</i> , 177(5):1152-1158 (1995)
X81379	dapE	Succinylidiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of <i>Corynebacterium glutamicum</i> complementing dapE of <i>Escherichia coli</i> ," <i>Microbiology</i> , 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus <i>Corynebacterium</i> deduced from analyses of small-subunit ribosomal DNA sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," <i>J. Bacteriol.</i> , 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus <i>Corynebacterium</i> based on 16S rRNA gene sequences," <i>Int. J. Syst. Bacteriol.</i> , 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of <i>Corynebacterium glutamicum</i> reveals the presence of aroP, which encodes the aromatic amino acid transporter," <i>J. Bacteriol.</i> , 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," <i>Microbiology</i> , 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," <i>Microbiology</i> , 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," <i>J. Bacteriol.</i> , 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from <i>Corynebacterium glutamicum</i> : cloning, molecular analysis and search for a consensus motif," <i>Microbiology</i> , 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of <i>Corynebacterium glutamicum</i> ," <i>J. Biol. Chem.</i> , 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the <i>Corynebacterium glutamicum</i> betP gene, encoding the transport system for the compatible solute glycine betaine," <i>J. Bacteriol.</i> , 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of <i>Corynebacterium glutamicum</i> , encoding two enzymes involved in L-lysine synthesis," <i>Biotechnol. Lett.</i> , 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrijic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from <i>Corynebacterium glutamicum</i> ," <i>Mol. Microbiol.</i> , 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," <i>Appl. Environ. Microbiol.</i> , 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," <i>Gene</i> , 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," <i>Nucleic Acids Res.</i> , 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," <i>Nucleic Acids Res.</i> , 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," <i>Mol. Microbiol.</i> , 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," <i>Mol. Gen. Genet.</i> , 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," <i>Arch. Microbiol.</i> , 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," <i>Microbiology</i> , 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," <i>Appl. Microbiol. Biotechnol.</i> , 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," <i>Microbiol.</i> , 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12337	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," <i>J. Bacteriol.</i> , 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," <i>FEMS Microbiol. Lett.</i> , 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynebacterium 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," <i>Virology</i> , 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," <i>J. Bacteriol.</i> , 175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," <i>J. Bacteriol.</i> , 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," <i>Appl. Environ. Microbiol.</i> , 60(7):2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al. "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," <i>Gene</i> , 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al. "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," <i>J. Bacteriol.</i> , 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," <i>Gene</i> , 170(1):91-94 (1996)

¹ A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	Species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCIC	DSMZ
Brevibacterium	ammoniaenes	21054							
Brevibacterium	ammoniaenes	19350							
Brevibacterium	ammoniaenes	19351							
Brevibacterium	ammoniaenes	19352							
Brevibacterium	ammoniaenes	19353							
Brevibacterium	ammoniaenes	19354							
Brevibacterium	ammoniaenes	19355							
Brevibacterium	ammoniaenes	19356							
Brevibacterium	ammoniaenes	21055							
Brevibacterium	ammoniaenes	21077							
Brevibacterium	ammoniaenes	21553							
Brevibacterium	ammoniaenes	21580							
Brevibacterium	ammoniaenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	flavum								
Brevibacterium	flavum								
Brevibacterium	flavum	21127							
Brevibacterium	flavum								
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum							70	
Brevibacterium	lactofermentum							74	
Brevibacterium	lactofermentum							77	
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum							B11470	
Brevibacterium	lactofermentum							B11471	
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum							11160	
Brevibacterium	spec.								717.73
Brevibacterium	spec.								717.73
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							

Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniaenes	6872						2399	
Corynebacterium	ammoniaenes	15511							
Corynebacterium	fujikense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrolophilus	21419					11594		
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japan.

TABLE 4: ALIGNMENT RESULTS

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rx00009	1023	GB_IN1:CELZK563	29655	U40061	Caenorhabditis elegans cosmid ZK563.	Caenorhabditis elegans	33,694	9-Nov-95
		GB_IN1:CELZK563	29655	U40061	Caenorhabditis elegans cosmid ZK563.	Caenorhabditis elegans	36,040	9-Nov-95
rx00010	810	GB_BA1:MTCY164	39150	Z95150	Mycobacterium tuberculosis H37Rv complete genome; segment 135/162.	Mycobacterium tuberculosis	38,442	19-Jun-98
		GB_BA1:MTFTSX	4068	X70031	M.tuberculosis ftsX and ftsE (partial) genes.	Mycobacterium tuberculosis	63,158	06-MAR-1997
		GB_BA1:SHGCP1R	107379	X86780	S.hydroscopius gene cluster for polyketide immunosuppressant rapamycin.	Streptomyces hygroscopicus	38,875	16-Aug-96
rx00024	1068	GB_HTG1:CEY113G7_3110000	AL031113	AL031113	Caenorhabditis elegans chromosome V clone Y113G7, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	36,217	12-Jan-99
		GB_HTG1:CEY113G7_3110000	AL031113	AL031113	Caenorhabditis elegans chromosome V clone Y113G7, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	36,217	12-Jan-99
		GB_PL2:ATF1C12	111945	AL022224	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSA project).	Arabidopsis thaliana	35,824	20-Sep-99
rx00048	1782	GB_HTG3:AC008905	129915	AC008905	Homo sapiens chromosome 5 clone CITB-H1_2259114, *** SEQUENCING IN PROGRESS ***; 40 unordered pieces.	Homo sapiens	38,826	3-Aug-99
		GB_HTG3:AC008905	129915	AC008905	Homo sapiens chromosome 5 clone CITB-H1_2259114, *** SEQUENCING IN PROGRESS ***; 40 unordered pieces.	Homo sapiens	38,826	3-Aug-99
		GB_HTG3:AC008905	129915	AC008905	Homo sapiens chromosome 5 clone CITB-H1_2259114, *** SEQUENCING IN PROGRESS ***; 40 unordered pieces.	Homo sapiens	37,379	3-Aug-99
rx00070	555	GB_BA2:BPEFUR	1003	L31851	Bordetella pertussis DNA repair protein (recN) gene, partial cds; iron regulatory protein (fur) gene, complete cds.	Bordetella pertussis	45,756	17-Apr-95
		GB_BA2:BPU11699	537	U11699	Bordetella pertussis ferric uptake regulator (fur) gene, complete cds.	Bordetella pertussis	47,119	14-Jan-95
		GB_BA1:BTFFURREC	1106	Z48227	B.pertussis fur gene for ferric uptake regulator and partial recN gene.	Bordetella pertussis	45,756	10-Feb-95
rx00078	537	GB_PR3:HUMCOL2A1Z31001	L10347	L10347	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds.	Homo sapiens	39,010	3-Aug-95
		GB_HTG2:AC006721	135550	AC006721	Caenorhabditis elegans clone Y18H1, *** SEQUENCING IN PROGRESS ***; 5 unordered pieces.	Caenorhabditis elegans	40,661	23-Feb-99
		GB_HTG2:AC006721	135550	AC006721	Caenorhabditis elegans clone Y18H1, *** SEQUENCING IN PROGRESS ***; 5 unordered pieces.	Caenorhabditis elegans	40,661	23-Feb-99
rx00088	899	GB_RO:MMCGT6	3009	U48896	Mus musculus UDP-galactose:ceramide galactosyltransferase (Cgt) gene, exon 6 and complete cds.	Mus musculus	35,455	1-Nov-96
		GB_RO:MMCGT6	3009	U48896	Mus musculus UDP-galactose:ceramide galactosyltransferase (Cgt) gene, exon 6 and complete cds.	Mus musculus	34,439	1-Nov-96
rx00100	723	GB_PL1:CAC41C10	38874	AL033501	C. albicans cosmid Ca41C10.	Candida albicans	36,222	10-Nov-98
		GB_PR4:AC007115	180821	AC007115	Homo sapiens chromosome 12 clone 91705, complete sequence.	Homo sapiens	33,050	17-Aug-99
		GB_PR4:AC007115	180821	AC007115	Homo sapiens chromosome 12 clone 91705, complete sequence.	Homo sapiens	34,993	17-Aug-99
rx00135	1377	GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	60,639	17-Jun-98
		GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	38,377	09-MAR-1995
		GB_BA1:MTMURAGEN1257	X96711	X96711	M.tuberculosis murA gene.	Mycobacterium tuberculosis	61,575	22-MAR-1996
rx00143	1605	GB_PAT:192051	1107	192051	Sequence 18 from patent US 5726299.	Unknown.	37,773	01-DEC-1998

TABLE 4: ALIGNMENT RESULTS

rx00177	1191	GB_PAT:178761	1107	I78761	Sequence 17 from patent US 5693781.	Unknown.	37,773	3-Apr-98
		GB_BA1:MTCY28	40163	Z95890	Mycobacterium tuberculosis H37Rv complete genome; segment 79/162.	Mycobacterium tuberculosis	36,984	18-Jun-98
		GB_GSS14:AQ543786	345	AQ543786	RPCL11-1-365L6. TV RPCL11 Homo sapiens genomic clone RPCL11-1-365L6, genomic survey sequence.	Homo sapiens	38,551	19-MAY-1999
		GB_PL2:AF017646	3394	AF017646	Schizosaccharomyces pombe TFIH subunit p47 (tfh47) gene, complete cds.	Schizosaccharomyces pombe	38,122	17-MAR-1999
		GB_PL1:SPCC1682	37404	AL031525	S.pombe chromosome III cosmid c1682.	Schizosaccharomyces pombe	33,983	14-DEC-1998
rx00178	1008	GB_BA1:AB016258	2260	AB016258	Arthrobacter sp. gene for maleylacetate reductase and hydroxyquinol 1,2-dioxygenase, partial and complete cds.	Arthrobacter sp.	65,182	8-Sep-99
		GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	38,806	8-Sep-97
rx00277	1684	GB_STS:G05495	271	G05495	human STS WI-5918.	Homo sapiens	39,925	8-Jun-95
		GB_BA1:MTCY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	39,976	17-Jun-98
		GB_IN1:CELT03F1	38643	U88169	Caenorhabditis elegans cosmid T03F1.	Caenorhabditis elegans	35,127	7-Feb-97
		GB_IN2:CELK02A2	38261	U23171	Caenorhabditis elegans cosmid K02A2.	Caenorhabditis elegans	36,166	21-MAY-1999
rx00372	1200	GB_IN2:AC005452	79333	AC005452	Drosophila melanogaster, chromosome 2R, region 43B2-43C2, P1 clone DS07185, complete sequence.	Drosophila melanogaster	37,006	26-Nov-98
		GB_IN2:AC005452	79333	AC005452	Drosophila melanogaster, chromosome 2R, region 43B2-43C2, P1 clone DS07185, complete sequence.	Drosophila melanogaster	34,907	26-Nov-98
rx00389	1683	GB_IN1:CELW03F8	34766	AF039041	Caenorhabditis elegans cosmid W03F8.	Caenorhabditis elegans	40,712	1-Jan-98
		GB_IN1:AB010703	772	AB010703	Theileria sp. gene for major piroplasm surface protein, partial cds, isolate Kamphaeng Saen.	Theileria sp.	40,285	18-Apr-98
		GB_BA1:LLU08911	619	U08911	Lactobacillus leichmannii putative D-alanine ligase (ddl) gene, partial cds.	Lactobacillus leichmannii	40,194	16-Feb-96
rx00467	792	GB_IN1:TPMS1	822	Z48740	T.parva Tpm1 gene for merozoite surface glycoprotein.	Theileria parva	38,902	15-MAY-1995
		GB_PR4:DJ293M10	202267	AF111167	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene.	Homo sapiens	37,995	7-Apr-99
		GB_PR4:DJ293M10	202267	AF111167	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene.	Homo sapiens	36,639	7-Apr-99
rx00499	1404	GB_IN1:CEW01C9	21493	Z49969	Caenorhabditis elegans cosmid W01C9, complete sequence.	Caenorhabditis elegans	37,980	23-Nov-98
		GB_PR4:AC007206	42732	AC007206	Homo sapiens chromosome 19, cosmid R27370, complete sequence.	Homo sapiens	34,982	4-Apr-99
		GB_EST26:AI344735	462	AI344735	qp05a10.x1 NCL_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917114 3' similar to gb:M15800 T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN (HUMAN); mRNA sequence.	Homo sapiens	42,675	2-Feb-99
rx00508	1206	GB_PR4:AC006479	161837	AC006479	Homo sapiens clone DJ1051J04, complete sequence.	Homo sapiens	38,462	11-Nov-99
		GB_HTG2:AC007111	84245	AC007111	Homo sapiens chromosome 16 clone 1-8F, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	37,931	18-MAR-1999
		GB_HTG2:AC007111	84245	AC007111	Homo sapiens chromosome 16 clone 1-8F, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	37,931	18-MAR-1999
		GB_Vi:AF141890	1791	AF141890	Columbid herpesvirus 1 DNA-dependent DNA polymerase gene, partial cds.	columbid herpesvirus 1	39,401	7-Jul-99
rx00569	1149	GB_PAT:115213	3728	I15213	Sequence 1 from patent US 5460951.	Unknown.	41,244	2-Apr-96
		GB_PAT:E07353	3728	E07353	cDNA encoding bone-related carboxypeptidase-like protein,OSF-5.	Mus sp.	41,244	29-Sep-97

TABLE 4: ALIGNMENT RESULTS

GB_HTG1:CEY70G10	152184	AL020987	Caenorhabditis elegans chromosome III clone Y70G10, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	34,148	12-DEC-1997
GB_HTG2:AC005020	177756	AC005020	Homo sapiens clone GS259H13, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.	Homo sapiens	34,551	12-Jun-98
GB_HTG2:AC005020	177756	AC005020	Homo sapiens clone GS259H13, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.	Homo sapiens	34,551	12-Jun-98
GB_HTG2:AC005020	177756	AC005020	Homo sapiens clone GS259H13, *** SEQUENCING IN PROGRESS *** , 4 unordered pieces.	Homo sapiens	37,628	12-Jun-98
GB_GSS15:AQ622921	517	AQ622921	HS_5351_A1_A08_T7A RPC1-11 Human Male BAC Library Homo sapiens genomic clone Plate=927 Col=15 Row=A, genomic survey sequence.	Homo sapiens	38,254	16-Jun-99
GB_GSS3:B36703	432	B36703	HS-1041-B1-B12-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=23 Row=D, genomic survey sequence.	Homo sapiens	44,981	17-OCT-1997
GB_EST25:A1245926	572	A1245926	qk33c08.x1 NCLCGAP_Co8 Homo sapiens cDNA clone IMAGE:1870766 3' similar to SW:COGP_BOVIN PS3620 COATOMER GAMMA SUBUNIT ;, mRNA sequence.	Homo sapiens	38,902	28-Jan-99
GB_EST1:D36491	360	D36491	CELK033GYF Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk33g11 5', mRNA sequence.	Caenorhabditis elegans	40,390	8-Aug-94
GB_IN2:CELC16A3	34968	U41534	Caenorhabditis elegans cosmid C16A3.	Caenorhabditis elegans	35,477	18-MAY-1999
GB_HTG3:AC009311	160198	AC009311	Homo sapiens clone NH0311L03, *** SEQUENCING IN PROGRESS *** , 3 unordered pieces.	Homo sapiens	38,636	13-Aug-99
GB_BA1:AB004795	3039	AB004795	Pseudomonas sp. gene for dipeptidyl aminopeptidase, complete cds.	Pseudomonas sp.	54,721	5-Feb-99
GB_BA1:MBOP11	2392	D38405	Moraxella lacunata gene for protease II, complete cds.	Moraxella lacunata	50,167	8-Feb-99
GB_IN2:AF078916	2960	AF078916	Trypanosoma brucei brucei oligopeptidase B (opb) gene, complete cds.	Trypanosoma brucei brucei	48,076	08-OCT-1999
GB_BA2:AF043741	1223	AF043741	Rhodococcus rhodochrous catechol 1,2-dioxygenase (catA) gene, complete cds.	Rhodococcus rhodochrous	66,940	27-Aug-98
GB_BA1:D83237	1626	D83237	Rhodococcus erythropolis DNA for catechol 1,2-dioxygenase, complete cds.	Rhodococcus erythropolis	65,440	1-Sep-99
GB_BA1:ROX99622	7224	X99622	Rhodococcus opacus catR, catA, catB, catC genes and five ORFs.	Rhodococcus opacus	63,617	24-Sep-97
GB_BA2:AF134348	5000	AF134348	Pseudomonas putida plasmid pDK1 toluate 1,2 dioxygenase subunit (xylX), toluate 1,2 dioxygenase subunit (xylY), and toluate 1,2 dioxygenase subunit (xylZ) genes, complete cds; and 1,2-dihydroxycyclohexa-3,5-diene carboxylate dehydrogenase (xylL) gene, partial cds.	Pseudomonas putida	59,863	20-MAY-1999
GB_BA1:PWVWXYL	9037	M64747	Pseudomonas putida plasmid pWW0 meta operon, 5' genes.	Plasmid pWW0	59,588	26-Apr-93
GB_BA1:PCCBDABC	3548	X79076	P. cepacia (2CBS) cbdA, cbdB and cbdC genes.	Burkholderia cepacia	55,410	3-Apr-97
GB_BA2:AF134348	5000	AF134348	Pseudomonas putida plasmid pDK1 toluate 1,2 dioxygenase subunit (xylX), toluate 1,2 dioxygenase subunit (xylY), and toluate 1,2 dioxygenase subunit (xylZ) genes, complete cds; and 1,2-dihydroxycyclohexa-3,5-diene carboxylate dehydrogenase (xylL) gene, partial cds.	Pseudomonas putida	60,920	20-MAY-1999
GB_BA1:PWVWXYL	9037	M64747	Pseudomonas putida plasmid pWW0 meta operon, 5' genes.	Plasmid pWW0	58,756	26-Apr-93
GB_GSS11:AQ274007	637	AQ274007	nbxb0032107f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0032107f, genomic survey sequence.	Oryza sativa	41,390	3-Nov-98

TABLE 4: ALIGNMENT RESULTS

rx00643	1659	GB_BA2:AF134348	5000	AF134348	Pseudomonas putida plasmid pDK1 toluate 1,2 dioxxygenase subunit (xyIX), Pseudomonas putida toluate 1,2 dioxxygenase subunit (xyIY), and toluate 1,2 dioxxygenase subunit (xyIZ) genes, complete cds; and 1,2-dihydroxycyclohexa-3,5-diene carboxylate dehydrogenase (xylL) gene, partial cds.	53,871	20-MAY-1999
rx00644	951	GB_BA1:PWVWXYL	9037	M64747	Pseudomonas putida plasmid pWW0 meta operon, 5' genes.	52,603 43,865	26-Apr-93 16-Jun-98
		GB_EST22:AI020666	328	AI020666	ua97f07.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:1365445 5' similar to SW:DUS7_RAT Q63340 DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 ; mRNA sequence.		
		GB_BA1:PWVWXYL	9037	M64747	Pseudomonas putida plasmid pWW0 meta operon, 5' genes.	55,626 50,410	26-Apr-93 20-MAY-1999
		GB_BA2:AF134348	5000	AF134348	Pseudomonas putida plasmid pDK1 toluate 1,2 dioxxygenase subunit (xyIX), Pseudomonas putida toluate 1,2 dioxxygenase subunit (xyIY), and toluate 1,2 dioxxygenase subunit (xyIZ) genes, complete cds; and 1,2-dihydroxycyclohexa-3,5-diene carboxylate dehydrogenase (xylL) gene, partial cds.		
rx00658	816	GB_EST22:AI038396	438	AI038396	ox21g10.x1 Soares_feta_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1657026 3' similar to contains Alu repetitive element; contains element L1 repetitive element ; mRNA sequence.	40,138	28-Aug-98
		GB_EST16:C26090	414	C26090	C26090 Rice callus cDNA Oryza sativa cDNA clone C11617_1A, mRNA sequence.	40,636	6-Aug-97
		GB_EST16:C26090	414	C26090	C26090 Rice callus cDNA Oryza sativa cDNA clone C11617_1A, mRNA sequence.	38,406	6-Aug-97
rx00663	1497	GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	57,976	24-Jun-99
		GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	39,669	27-Aug-99
		GB_HTG2:AC007482	155357	AC007482	Homo sapiens clone hRPK.56_A_1, *** SEQUENCING IN PROGRESS ***, Homo sapiens 6 unordered pieces.	36,154	05-MAY-1999
		GB_BA1:SC3C8	33095	AL023861	Streptomyces coelicolor cosmid 3C8.	36,836	15-Jan-99
rx00675	915	GB_PR3:AC005736	215441	AC005736	Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.	42,027	01-OCT-1998
		GB_IN2:AC005719	188357	AC005719	Drosophila melanogaster, chromosome 2L, region 38A5-38B4, BAC clone BACR48M05, complete sequence.	35,531	27-OCT-1999
rx00762	999	GB_HTG2:HSJ473J16	203460	AL109942	Homo sapiens chromosome 6 clone RP3-473J16 map q25.3-26, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	37,295	03-DEC-1999
		GB_HTG2:HSJ473J16	203460	AL109942	Homo sapiens chromosome 6 clone RP3-473J16 map q25.3-26, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	37,295	03-DEC-1999
rx00772	1629	GB_PR2:HSU91327	129252	U91327	Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.	35,650	21-Aug-97
		GB_BA2:AF010184	1494	AF010184	Pseudomonas aeruginosa coenzyme A transferase PsecoA (psecoA) gene, complete cds.	56,472	18-Jul-98
rx00778	1248	GB_PAT:I92043	713	I92043	Sequence 10 from patent US 5726299.	92,701	01-DEC-1998
		GB_PAT:I78754	713	I78754	Sequence 10 from patent US 5693781.	92,701	3-Apr-98
		GB_BA1:MTFST2GN	1347	Z48056	M.tuberculosis PstS-2 gene.	47,791	24-Apr-99
		GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885.	35,536	7-Feb-99
		GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885.	38,006	7-Feb-99

TABLE 4: ALIGNMENT RESULTS

rx00787	2025	GB_PL1:SCX11RA	36849	X91258	S.cerevisiae DNA from chromosome XII right arm including ACE2, CK11, PDC5, SLS1, PUT1 and tRNA-Asp genes.	Saccharomyces cerevisiae	36,122	13-OCT-1995
		GB_PL2:YSC19606	29154	U53881	Saccharomyces cerevisiae chromosome XII cosmid 9606.	Saccharomyces cerevisiae	36,122	25-OCT-1997
		GB_PL1:SCX11RA	36849	X91258	S.cerevisiae DNA from chromosome XII right arm including ACE2, CK11, PDC5, SLS1, PUT1 and tRNA-Asp genes.	Saccharomyces cerevisiae	37,198	13-OCT-1995
rx00792	1320	GB_PR4:AC004841	132072	AC004841	Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.	Homo sapiens	37,452	18-MAR-1999
		GB_HTG2:AC006706	180664	AC006706	Caenorhabditis elegans clone Y110A2, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Caenorhabditis elegans	34,824	23-Feb-99
		GB_HTG2:AC006706	180664	AC006706	Caenorhabditis elegans clone Y110A2, *** SEQUENCING IN PROGRESS ***; 4 unordered pieces.	Caenorhabditis elegans	34,824	23-Feb-99
rx00857	1313	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	38,080	17-Jun-98
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	68,345	03-DEC-1996
		GB_BA1:MLCB33	42224	Z94723	Mycobacterium leprae cosmid B33.	Mycobacterium leprae	38,824	24-Jun-97
rx00877	1788	GB_PAT:192050	567	I92050	Sequence 17 from patent US 5726299.	Unknown.	62,787	01-DEC-1998
		GB_PAT:178760	567	I78760	Sequence 16 from patent US 5693781.	Unknown.	62,787	3-Apr-98
		GB_BA2:AE000426	10240	AE000426	Escherichia coli K-12 MG1655 section 316 of 400 of the complete genome.	Escherichia coli	36,456	12-Nov-98
rx00888	1140	GB_BA1:MTCY27	27548	Z95208	Mycobacterium tuberculosis H37Rv complete genome; segment 104/162.	Mycobacterium tuberculosis	40,165	17-Jun-98
		GB_BA1:U00016	42931	U00016	Mycobacterium leprae cosmid B1937.	Mycobacterium leprae	58,444	01-MAR-1994
		GB_BA1:ECU82598	136742	U82598	Escherichia coli genomic sequence of minutes 9 to 12.	Escherichia coli	37,876	15-Jan-97
rx00892	1017	GB_BA2:AE000817	13157	AE000817	Methanobacterium thermoautotrophicum from bases 251486 to 264642 (section 23 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	36,710	15-Nov-97
		GB_EST29:AI620549	239	AI620549	tu95b07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2258773 3' similar to gb:X60708_rna1 DIPEPTIDYL PEPTIDASE IV (HUMAN);, mRNA sequence.	Homo sapiens	38,075	21-Apr-99
		GB_BA2:AE000817	13157	AE000817	Methanobacterium thermoautotrophicum from bases 251486 to 264642 (section 23 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	35,650	15-Nov-97
rx00897	1128	GB_PR3:HS246D7	28011	AL031843	Human DNA sequence from clone 246D7 on chromosome 22q13.1-13.33. Contains ESTs, a GSS and an STS, complete sequence.	Homo sapiens	38,724	23-Nov-99
		GB_PR3:HSDJ185D5	24387	AL118498	Human DNA sequence from clone 185D5 on chromosome 22, complete sequence.	Homo sapiens	37,021	23-Nov-99
		GB_PR3:HS246D7	28011	AL031843	Human DNA sequence from clone 246D7 on chromosome 22q13.1-13.33. Contains ESTs, a GSS and an STS, complete sequence.	Homo sapiens	36,054	23-Nov-99
rx00944	1095	GB_BA1:ECU68759	1531	U68759	Enterobacter cloacae pentaerythritol tetranitrate reductase (onr) gene, complete cds.	Enterobacter cloacae	43,041	14-DEC-1996
		GB_PAT:A59288	1531	A59288	Sequence 1 from Patent WO9703201.	unidentified	43,041	06-MAR-1998
		GB_EST23:AI099394	601	AI099394	ue32a09.y1 Sugano mouse liver mila Mus musculus c-met tyrosine kinase receptor mRNA, complete (MOUSE);, mRNA sequence. IMAGE:1482040 5' similar to gb:U21301 Mus musculus c-met tyrosine	Mus musculus	37,225	20-Aug-98
rx00954	1248	GB_HTG6:AC009794	152794	AC009794	Homo sapiens chromosome 4 clone RP11-343C10 map 4, *** SEQUENCING IN PROGRESS ***; 33 unordered pieces.	Homo sapiens	34,762	03-DEC-1999
		GB_HTG6:AC009794	152794	AC009794	Homo sapiens chromosome 4 clone RP11-343C10 map 4, *** SEQUENCING IN PROGRESS ***; 33 unordered pieces.	Homo sapiens	35,708	03-DEC-1999

TABLE 4: ALIGNMENT RESULTS

rx00982	1629	GB_BA1:BLARGS	2501	Z21501	B.lactofermentum argS and lysA genes for arginyl-tRNA synthetase and diaminopimelate decarboxylase (partial).	Corynebacterium glutamicum 39,003	28-DEC-1993
		GB_BA1:CGXLYSA	2344	X54740	Corynebacterium glutamicum argS-lysA operon gene for the upstream region of the arginyl-tRNA synthetase and diaminopimelate decarboxylase (EC 4.1.1.20).	Corynebacterium glutamicum 41,435	30-Jun-93
		GB_PAT:E14508	3579	E14508	DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-tRNA synthase.	Corynebacterium glutamicum 40,566	28-Jul-99
rx01014	2724	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis 56,167	17-Jun-98
		GB_BA1:STMAMPEPN	2849	L23172	Streptomyces lividans aminopeptidase N gene, complete cds.	Streptomyces lividans 57,067	18-MAY-1994
		GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2.	Streptomyces coelicolor 37,551	2-Aug-99
rx01022	1203	GB_PAT:A68384	1080	A68384	Sequence 1 from Patent WO9748809.	Mycobacterium avium 56,913	06-MAY-1999
		GB_BA2:AF077728	1346	AF077728	Mycobacterium smegmatis D-alanine ligase gene, complete cds.	Mycobacterium smegmatis 57,203	1-Jan-99
rx01055		GB_BA1:MSG81723CS	38477	L78825	Mycobacterium leprae cosmid B1723 DNA sequence.	Mycobacterium leprae 54,599	15-Jun-96
rx01056	1023	GB_BA2:AE001715	11086	AE001715	Thermotoga maritima section 27 of 136 of the complete genome.	Thermotoga maritima 39,034	2-Jun-99
		GB_EST38:AW046857	161	AW046857	U1-M-BH1-aki-a-04-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone	Mus musculus 45,963	18-Sep-99
		GB_EST38:AW049435	244	AW049435	U1-M-BH1-aki-a-04-0-UI 3', mRNA sequence.		
		GB_PL1:LPAJ5046	656	AJ225046	U1-M-BH1-ams-b-01-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone	Mus musculus 40,984	18-Sep-99
		GB_PL2:SPAC806	22870	AL117212	U1-M-BH1-ams-b-01-0-UI 3', mRNA sequence.		
rx01057	1626	GB_PL1:LPAJ5046	656	AJ225046	Lycopersicon peruvianum mRNA for Hsp20.1 protein.	Lycopersicon peruvianum 37,117	22-Jul-98
		GB_PL2:SPAC806	22870	AL117212	S.pombe chromosome I cosmid c806.	Schizosaccharomyces pombe 38,211	24-Nov-99
		GB_PL2:SPAC806	22870	AL117212	S.pombe chromosome I cosmid c806.	Schizosaccharomyces pombe 36,934	24-Nov-99
rx01082	783	GB_BA2:AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum 99,794	5-Aug-99
		GB_PL2:TAE237897	8020	AJ237897	Triticum aestivum sbe1 gene, exons 1-14.	Triticum aestivum 37,132	1-Nov-99
		GB_PL2:AF076680	10499	AF076680	Aegilops tauschii starch branching enzyme-1 (SBE-1) gene, complete cds.	Aegilops tauschii 38,651	14-MAY-1999
rx01113	260	GB_VI:ASU02468	11424	U02468	African swine fever virus BA71V (A489R, A280R, A505R, A498R, A528R, A506R, and A542R) genes, complete cds.	African swine fever virus 31,923	28-Apr-94
		GB_VI:ASU18466	170101	U18466	African swine fever virus, complete genome.		
		GB_GSS5:AQ752779	1647	AQ752779	HS_5569_B1_D02_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1145 Col=3 Row=H, genomic survey sequence.	African swine fever virus 31,923	22-Apr-95
rx01115	876	GB_BA1:AB014757	6057	AB014757	Pseudomonas sp. 61-3 genes for PhbR, acetylacetyl-CoA reductase, beta-ketothiolase and PHB synthase, complete cds.	Homo sapiens 37,154	19-Jul-99
		GB_IN2:DMU60591	5630	U60591	Drosophila melanogaster kuzbanian (kuz) mRNA, complete cds.	Pseudomonas sp. 61-3 40,850	26-DEC-1998
		GB_RO:MMMP10	1744	Y13185	Mus musculus mRNA for stromelysin-2.	Drosophila melanogaster 37,326	10-Sep-96
rx01116	735	GB_BA1:SC4C6	30941	AL079355	Streptomyces coelicolor cosmid 4C6.	Mus musculus 35,877	14-Jan-98
		GB_BA2:AF109386	6551	AF109386	Streptomyces coelicolor cosmid 4C6.	Streptomyces coelicolor 40,616	21-Jun-99
		GB_BA1:MTCY07A7	23967	Z95556	Streptomyces sp. 2065 protocatechuic acid catabolic gene cluster, complete sequence.	Streptomyces sp. 2065 64,099	06-DEC-1999
		GB_BA1:MTCY07A7	23967	Z95556	Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.	Mycobacterium tuberculosis 41,716	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

rx01117	864	GB_BA2:AF109386	6551	AF109386	Streptomyces sp. 2065 complete sequence.	Streptomyces sp. 2065	62,116	06-DEC-1999
		GB_BA2:AF003947	5475	AF003947	Rhodococcus opacus succinyl CoA:3-oxoadipate CoA transferase subunit homolog (pcaI) gene, partial cds, protocatechuate dioxygenase beta subunit (pcaH), protocatechuate dioxygenase alpha subunit (pcaG), 3-carboxy-cis-muconate cycloisomerase homolog (pcaB), 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase (pcaL) and PcaR (pcaR) genes, complete cds, and 3-oxoadipyl CoA thiolase homolog (pcaF) gene, partial cds.	Rhodococcus opacus	36,712	12-MAR-1998
rx01120	1401	GB_BA1:XCLPSIJ	2578	Y11313	X.campestris lpsI, lpsJ, xanA genes and orfX.	Xanthomonas campestris	39,833	20-Jan-98
		GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	36,715	17-Jun-98
		GB_BA1:CAJ10321	6710	AJ010321	Caulobacter crescentus partial tig gene and clpP, ctaA, clpX, lon genes.	Caulobacter crescentus	63,311	01-OCT-1998
		GB_BA2:AF150957	4440	AF150957	Azospirillum brasilense trigger factor (tig), heat-shock protein ClpP (clpP), and heat-shock protein ClpX (clpX) genes, complete cds; and Lon protease (lon) gene, partial cds.	Azospirillum brasilense	60,613	7-Jun-99
rx01126	583	GB_HTG3:AC009199	66498	AC009199	Drosophila melanogaster chromosome 2 clone BACR10J23 (D1024) RPCI-98 10.J.23 map 37B-37B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.	Drosophila melanogaster	35,294	20-Sep-99
		GB_HTG3:AC009199	66498	AC009199	Drosophila melanogaster chromosome 2 clone BACR10J23 (D1024) RPCI-98 10.J.23 map 37B-37B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.	Drosophila melanogaster	35,294	20-Sep-99
		GB_PL1:AB016880	81284	AB016880	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence.	Arabidopsis thaliana	34,477	20-Nov-99
rx01181	980	GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	61,570	22-Aug-97
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	60,434	17-Jun-98
		GB_BA1:SC5F7	40024	AL096872	Streptomyces coelicolor cosmid 5F7.	Streptomyces coelicolor	57,011	22-Jul-99
rx01236	1068	GB_EST3:H01832	381	H01832	yj28c11.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150068 3', mRNA sequence.	A3(2) Homo sapiens	41,406	19-Jun-95
		GB_PR4:AC004850	105891	AC004850	Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.	Homo sapiens	37,428	26-Feb-99
		GB_GSS11:AQ304150	528	AQ304150	HS_3208_A1_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=23 Row=G, genomic survey sequence.	Homo sapiens	37,421	16-DEC-1998
rx01254	1392	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	58,315	24-Jun-99
		GB_BA1:MSGB577COS3770		L01263	M. leprae genomic dna sequence, cosmid b577.	Mycobacterium leprae	56,323	14-Jun-96
		GB_BA1:MLCB2407	35615	AL023596	Mycobacterium leprae cosmid B2407.	Mycobacterium leprae	37,645	27-Aug-99
rx01270	1278	GB_BA1:BSPX91182	345	X91182	Bacterial sp. partial 16S rRNA gene (clone group G10).	unidentified bacterium	41,228	15-Jul-96
		GB_BA1:BSPJN12D	347	Z69277	Bacterial sp. partial 16S rRNA gene (clone group JN12d).	Bacteria	38,905	24-Jun-98
		GB_EST7:W93397	545	W93397	zd95b03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357197 3', mRNA sequence.	Homo sapiens	40,516	25-Nov-96
rx01277	2127	GB_PL2:AF111709	52684	AF111709	Oryza sativa subsp. indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete sequences; and unknown genes.	Oryza sativa subsp. indica	37,410	26-Apr-99
		GB_IN1:CELZC250	34372	AF003383	Caenorhabditis elegans cosmid ZC250.	Caenorhabditis elegans	35,506	14-MAY-1997

TABLE 4: ALIGNMENT RESULTS

rx01288	498	GB_EST1:Z14808	331	Z14808	CEL5E4 Chris Martin sorted cDNA library <i>Caenorhabditis elegans</i> cDNA clone cm5e4.5', mRNA sequence.	<i>Caenorhabditis elegans</i>	36,890	19-Jun-97
		GB_VI:S62819	3348	S62819	F2L=putative RNA polymerase-associated transcription factor... F4R=type I orf virus topoisomerase homolog [orf virus OV, NZ2, host=sheep, Genomic, 3 genes, 3348 nt].		40,471	25-Aug-93
		GB_PR4:HUMCCLEC1	17079	AF077344	Homo sapiens cartilage-derived C-type lectin (CLECSF1) gene, exons 1 and 2.	Homo sapiens	34,631	15-OCT-1999
		GB_PR4:HUMCCLEC1	17079	AF077344	Homo sapiens cartilage-derived C-type lectin (CLECSF1) gene, exons 1 and 2.	Homo sapiens	39,300	15-OCT-1999
rx01354	1059	GB_PR1:D87675	301692	D87675	Homo sapiens DNA for amyloid precursor protein, complete cds.	Homo sapiens	37,984	22-Sep-97
		GB_PR1:D87675	301692	D87675	Homo sapiens DNA for amyloid precursor protein, complete cds.	Homo sapiens	35,140	22-Sep-97
		GB_RO:MMNUCLEO	11478	X07699	Mouse nucleolin gene.	Mus musculus	37,146	27-Aug-98
rx01376	984	GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,496	10-Feb-99
		GB_BA1:ACCP5XM	2748	X81320	A.calcoaceticus epsX and epsM genes.	Acinetobacter calcoaceticus	40,353	19-OCT-1994
		GB_BA2:ECU05248	1781	U05248	Escherichia coli polysialic acid gene cluster region 2 (neuD and neuB) genes, complete cds.	Escherichia coli	34,995	1-Feb-95
rx01385	2004	GB_BA1:FVBPENTA	2519	M98557	Flavobacterium sp. pentachlorophenol 4-monoxygenase gene, complete mRNA.	Flavobacterium sp.	40,855	26-Apr-93
		GB_PAT:119994	2516	I19994	Sequence 2 from patent US 5512478.	Unknown.	40,855	07-OCT-1996
		GB_BA2:AF059680	2410	AF059680	Sphingomonas sp. UG30 pentachlorophenol 4-monoxygenase (pcpB) gene, complete cds; and pentachlorophenol 4-monoxygenase reductase (pcpD) gene, partial cds.	Sphingomonas sp. UG30	42,993	27-Apr-99
rx01426	750	GB_GSS3:B35912	313	B35912	HS-1031-A2-D02-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 811 Col=4 Row=G, genomic survey sequence.	Homo sapiens	38,019	17-OCT-1997
		GB_GSS1:FR0027767	497	AL020589	F.rubripes GSS sequence, clone 197B17aA3, genomic survey sequence.	Fugu rubripes	35,814	10-DEC-1997
		GB_GSS5:AQ774340	449	AQ774340	HS_3137_A2_E11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=22 Row=I, genomic survey sequence.	Homo sapiens	40,535	29-Jul-99
rx01427	1044	GB_BA2:AF036766	3487	AF036766	Lactobacillus reuteri plasmid pTE15 replication-associated protein A (repA) and replication-associated protein B (repB) genes, complete cds.	Lactobacillus reuteri	39,101	19-Feb-98
		GB_PR4:AC007032	126803	AC007032	Homo sapiens clone NH0022N19, complete sequence.	Homo sapiens	34,180	17-Jul-99
		GB_PR4:AC007032	126803	AC007032	Homo sapiens clone NH0022N19, complete sequence.	Homo sapiens	36,858	17-Jul-99
rx01428	1260	GB_BA1:SCH24	41625	AL049826	Streptomyces coelicolor cosmid H24.	Streptomyces coelicolor	51,278	11-MAY-1999
		GB_BA2:AF031590	6676	AF031590	Streptomyces coelicolor thioredoxin (trxA) gene, partial cds; SpoOJ-like, Soj-Streptomyces coelicolor like, GidB-like, Jag-like, inner membrane protein, and 9-10kDa protein-like genes, complete cds; RNase P protein (mpA) gene, partial cds; and unknown gene.	Streptomyces coelicolor	39,389	20-Feb-98
		GB_BA1:SCTRXARNP	6676	Y16311	Streptomyces coelicolor trxA & mpA genes & ORFs 205, 344, 255, 239, 170, 341 & 124.	Streptomyces coelicolor	39,389	18-DEC-1998
rx01430	1311	GB_EST30:AI643302	254	AI643302	v139b08.y1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:974583 5' similar to SW:6PGD_HUMAN P52209 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING ;, mRNA sequence.	Mus musculus	38,627	29-Apr-99

TABLE 4: ALIGNMENT RESULTS

GB_EST34:AI788121	490	AI788121	AI788121	490	AI788121	u117f02.y1 Sugano mouse embryo meva Mus musculus cDNA clone IMAGE:2087835 5' similar to SW:6PGD_HUMAN P52209 6- PHOSPHOGLUCONATE DEHYDROGENASE; DECARBOXYLATING ; mRNA sequence.	Mus musculus	40,583	2-Jul-99
GB_EST16:AA560354	253	AA560354	AA560354	253	AA560354	v139b08.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:974583 5' similar to TR:G984325 G984325 PHOSPHOGLUCONATE DEHYDROGENASE ; mRNA sequence.	Mus musculus	42,544	18-Aug-97
GB_EST22:AI069195	892	AI069195	AI069195	892	AI069195	mgae0005dF02f Magnaporthe grisea Appressorium Stage cDNA Library Pyricularia grisea cDNA clone mgae0005dF02f 5' mRNA sequence.	Pyricularia grisea	40,964	09-DEC-1999
GB_EST26:AI392390	574	AI392390	AI392390	574	AI392390	NCSC1B12T7 Subtracted Conidial Neurospora crassa cDNA clone SC1B12 Neurospora crassa 3' similar to adenylate kinase 2 (ATP-AMP transphosphorylase), mRNA sequence.	Neurospora crassa	40,127	3-Feb-99
GB_HTG2:AC004845	140230	AC004845	AC004845	140230	AC004845	Homo sapiens clone DJ0635005, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	Homo sapiens	36,437	12-Jun-98
GB_BA1:CGPTAACKA 3657	3657	X89084	X89084	3657	X89084	C.glutamicum pta gene and ackA gene.	Corynebacterium glutamicum	100,000	23-MAR-1999
GB_BA1:MTCY22G10	35420	Z84724	Z84724	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	54,867	17-Jun-98
GB_HTG3:AC010254	114363	AC010254	AC010254	114363	AC010254	Homo sapiens chromosome 5 clone CIT-HSPC_434011, *** SEQUENCING IN PROGRESS ***; 58 unordered pieces.	Homo sapiens	35,547	15-Sep-99
GB_BA2:AF003947	5475	AF003947	AF003947	5475	AF003947	Rhodococcus opacus succinyl CoA:3-oxoadipate CoA transferase subunit homolog (pcaI') gene, partial cds, protocatechuate dioxygenase beta subunit (pcaH), protocatechuate dioxygenase alpha subunit (pcaG), 3-carboxy-cis-muconate cycloisomerase homolog (pcaB), 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase (pcaL) and PcaR (pcaR) genes, complete cds, and 3-oxoadipyl CoA thiolase homolog (pcaF') gene, partial cds.	Rhodococcus opacus	57,939	12-MAR-1998
GB_PR2:HSA535K18	182408	AL078638	AL078638	182408	AL078638	Human DNA sequence from clone RP11-535K18 on chromosome Xq26.2-27.1, complete sequence.	Homo sapiens	37,123	22-Nov-99
GB_EST33:AI764654	420	AI764654	AI764654	420	AI764654	UI-R-Y0-abw-e-02-Q-UI.s2 UI-R-Y0 Rattus norvegicus cDNA clone UI-R-Y0-abw-e-02-Q-UI 3' mRNA sequence.	Rattus norvegicus	35,885	25-Jun-99
GB_BA2:AF003947	5475	AF003947	AF003947	5475	AF003947	Rhodococcus opacus succinyl CoA:3-oxoadipate CoA transferase subunit homolog (pcaI') gene, partial cds, protocatechuate dioxygenase beta subunit (pcaH), protocatechuate dioxygenase alpha subunit (pcaG), 3-carboxy-cis-muconate cycloisomerase homolog (pcaB), 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase (pcaL) and PcaR (pcaR) genes, complete cds, and 3-oxoadipyl CoA thiolase homolog (pcaF') gene, partial cds.	Rhodococcus opacus	66,667	12-MAR-1998
GB_BA1:SC4C6	30941	AL079355	AL079355	30941	AL079355	Streptomyces coelicolor cosmid 4C6.	Streptomyces coelicolor	40,822	21-Jun-99
GB_BA2:AF109386	6551	AF109386	AF109386	6551	AF109386	Streptomyces sp. 2065 protocatechualic acid catabolic gene cluster, complete sequence.	Streptomyces sp. 2065	56,049	06-DEC-1999
GB_BA1:AB009343	6342	AB009343	AB009343	6342	AB009343	Frateruia sp. ANA-18 ORF2, catBI, catCI, catAI and catD genes, complete Frateruia sp. ANA-18 cds.	Frateruia sp. ANA-18	50,966	26-MAY-1999
GB_GSS10:AQ241375	284	AQ241375	AQ241375	284	AQ241375	CITBI-E1-250507.TF.1 CITBI-E1 Homo sapiens genomic clone 250507, genomic survey sequence.	Homo sapiens	39,085	30-Sep-98

TABLE 4: ALIGNMENT RESULTS

rx01465	1284	GB_HTG3:AC010363	174962	AC010363	Homo sapiens chromosome 5 clone CITB-H1_2039P12, *** SEQUENCING IN PROGRESS ***. 43 unordered pieces.	Homo sapiens	35,784	15-Sep-99
		GB_BA1:ROX99622	7224	X99622	Rhodococcus opacus catR, catA, catB, catC genes and five ORFs.	Rhodococcus opacus	58,814	24-Sep-97
		GB_BA1:D83237	1626	D83237	Rhodococcus erythropolis DNA for catechol 1,2-dioxygenase, complete cds.	Rhodococcus erythropolis	53,904	1-Sep-99
		GB_EST9:AA119571	445	AA119571	mp68d04.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:574375 5' similar to TR:G559375 G559375 RAS GTPASE-ACTIVATING PROTEIN. ; mRNA sequence.	Mus musculus	39,551	17-Feb-97
rx01466	1083	GB_EST37:AI934978	425	AI934978	wd17b06.x1 Soares_NFL_I_GBC_S1 Homo sapiens cDNA clone IMAGE:2328371 3' mRNA sequence.	Homo sapiens	43,609	2-Sep-99
		GB_EST15:AA465729	289	AA465729	aa32g06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE:815002 3' mRNA sequence.	Homo sapiens	41,115	13-Aug-97
		GB_EST24:AI219091	633	AI219091	qg12a05.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE:1759280 3' similar to TR:Q99988 Q99988 TGF-BETA SUPERFAMILY PROTEIN. [1] ; mRNA sequence.	Homo sapiens	36,066	29-Nov-98
rx01477	1671	GB_BA2:CGU89648	1105	U89648	Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence.	Corynebacterium glutamicum	49,726	30-MAR-1999
		GB_EST21:AA919685	782	AA919685	vx11g06.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:1264186 5' similar to gb:M73696 Murine Givri-1 mRNA, complete cds (MOUSE); mRNA sequence.	Mus musculus	37,762	20-Apr-98
rx01499	3945	GB_HTG2:HS1005F21	101795	AL078633	Homo sapiens chromosome 20 clone RP5-1005F21, *** SEQUENCING IN PROGRESS ***. in unordered pieces.	Homo sapiens	38,371	30-Nov-99
		GB_PR4:AC006454	153201	AC006454	Homo sapiens clone DJ0852P06, complete sequence.	Homo sapiens	38,033	13-Aug-99
		GB_BA1:LSLYSSYNT	4724	X96558	Lysobacter sp. gene encoding synthetase.	Lysobacter	42,840	8-Jan-97
		GB_PR4:AC006454	153201	AC006454	Homo sapiens clone DJ0852P06, complete sequence.	Homo sapiens	38,823	13-Aug-99
rx01502	1356	GB_PAT:192046	2203	I92046	Sequence 13 from patent US 5726299.	Unknown.	39,755	01-DEC-1998
		GB_PAT:178757	2203	I78757	Sequence 13 from patent US 5693781.	Unknown.	39,755	3-Apr-98
		GB_BA1:MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162.	Mycobacterium tuberculosis	36,613	17-Jun-98
rx01509	597	GB_BA1:SCE9	37730	AL049841	Streptomyces coelicolor cosmid E9.	Streptomyces coelicolor	60,637	19-MAY-1999
		GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome; segment 154/162.	Mycobacterium tuberculosis	59,296	17-Jun-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	59,764	27-Aug-99
rx01510	1404	GB_GSS9:AQ129927	440	AQ129927	HS_2165_B1_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=17 Row=H, genomic survey sequence.	Homo sapiens	36,136	23-Sep-98
		GB_BA2:AF016585	41097	AF016585	Streptomyces caelestis cytochrome P-450 hydroxylase homolog (nidI) gene, partial cds; polyketide synthase modules 1 through 7 (nidA) genes, complete cds; and N-methyltransferase homolog gene, partial cds.	Streptomyces caelestis	37,464	07-DEC-1997
		GB_HTG4:AC010747	216500	AC010747	Homo sapiens chromosome unknown clone NH0555H09, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	33,022	29-OCT-1999
rx01511	1065	GB_BA1:BRLBIOBA	1647	D14084	Brevibacterium flavum gene for biotin synthetase, complete cds.	Corynebacterium glutamicum	40,283	3-Feb-99
		GB_GSS3:B45213	358	B45213	HS-1060-B2-D07-MF.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 782 Col=14 Row=H, genomic survey sequence.	Homo sapiens	49,505	21-OCT-1997

TABLE 4: ALIGNMENT RESULTS

rx01513	2682	GB_HTG4:AC010747	216500	AC010747	Homo sapiens chromosome unknown clone NH0555H09, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	33,819	29-OCT-1999
		GB_BA1:MTCY7H7B	24244	Z95557	Mycobacterium tuberculosis H37Rv complete genome, segment 153/162.	Mycobacterium tuberculosis	40,354	18-Jun-98
		GB_BA2:AF037269	2364	AF037269	Mycobacterium smegmatis cell division protein (FtsH) gene, complete cds.	Mycobacterium smegmatis	60,814	19-Aug-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548.	Mycobacterium leprae	39,992	27-Aug-99
rx01593	990	GB_BA1:U00012	33312	U00012	Mycobacterium leprae cosmid B1308.	Mycobacterium leprae	39,126	30-Jan-96
		GB_IN1:CELF27E11	25700	AF016413	Caenorhabditis elegans cosmid F27E11.	Caenorhabditis elegans	34,227	2-Aug-97
		GB_OV:DYGAGR	4354	L01423	Discopige ommata (clone OL4) agrin mRNA, 3' end cds.	Discopige ommata	38,414	28-Apr-93
rx01608	1962	GB_BA2:AF119150	18605	AF119150	Vibrio cholerae Rtx toxin gene cluster, complete cds.	Vibrio cholerae	36,919	21-MAR-1999
		GB_BA2:AF119150	18605	AF119150	Vibrio cholerae Rtx toxin gene cluster, complete cds.	Vibrio cholerae	38,130	21-MAR-1999
rx01620								
rx01640	3441	GB_PR3:HS52D1	148691	Z96811	Human DNA sequence from PAC 52D1 on chromosome Xq21. Contains CA repeats, STS.	Homo sapiens	35,501	23-Nov-99
		GB_BA2:AF079155	686	AF079155	Ralstonia eutropha phasin (phaP) mRNA, complete cds.	Ralstonia eutropha	40,497	6-Apr-99
		GB_IN2:AF039570	1866	AF039570	Caenorhabditis elegans aryl hydrocarbon receptor ortholog AHR-1 (ahr-1) mRNA, complete cds.	Caenorhabditis elegans	39,699	04-OCT-1999
rx01653	1584	GB_HTG7:AC010997	187768	AC010997	Homo sapiens clone RP11-399K21, *** SEQUENCING IN PROGRESS ***	Homo sapiens	34,516	08-DEC-1999
		GB_HTG7:AC010997	187768	AC010997	35 unordered pieces.	Homo sapiens	36,177	08-DEC-1999
		GB_VI:AF030154	34446	AF030154	Bovine adenovirus 3 complete genome.	bovine adenovirus type 3	40,345	27-Jan-99
rx01716	509	GB_BA1:AB010645	16836	AB010645	Acetobacter xylinus genes for endoglucanase, cellulose synthase subunit ABCD and beta-glucosidase, complete cds.	Acetobacter xylinus	34,783	13-Feb-99
		GB_BA1:AB010645	16836	AB010645	Acetobacter xylinus genes for endoglucanase, cellulose synthase subunit ABCD and beta-glucosidase, complete cds.	Acetobacter xylinus	37,598	13-Feb-99
		GB_BA1:ABCB5ABCD9540		M37202	A.xylinum bcs A, B, C and D genes, complete cds's.	Acetobacter xylinus	39,173	24-Apr-93
rx01728	1098	GB_BA2:CORCSLYS	2821	M89931	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake carrier (brnQ) genes, complete cds, and hypothetical protein YhbW (yhbW) gene, partial cds.	Corynebacterium glutamicum	99,636	4-Jun-98
		GB_PL2:HAAP	931	X95952	H.annuus mRNA for aquaporin.	Helianthus annuus	39,231	14-Jul-99
		GB_HTG1:CEY32F6	187816	AL008875	Caenorhabditis elegans chromosome V clone Y32F6, *** SEQUENCING IN PROGRESS ***; in unordered pieces.	Caenorhabditis elegans	37,431	9-Nov-97
rx01732	1173	GB_PR4:HUAC004125	194020	AC004125	Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.	Homo sapiens	35,345	23-Nov-99
		GB_PR4:HUAC004125	194020	AC004125	Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.	Homo sapiens	37,381	23-Nov-99
		GB_IN1:CER11A5	26671	Z83122	Caenorhabditis elegans cosmid R11A5, complete sequence.	Caenorhabditis elegans	36,140	2-Sep-99
rx01810	1200	GB_EST28:AI499508	403	AI499508	to02d01.x1 NCI_CGAP_U12 Homo sapiens cDNA clone IMAGE:2177857 3' similar to SW:NU4M_PANTR P03906 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4.; mRNA sequence.	Homo sapiens	36,725	11-MAR-1999

TABLE 4: ALIGNMENT RESULTS

rx01828	1545	GB_EST28:AI499508	403	AI499508	to02d01.x1 NCI CGAP_U12 Homo sapiens cDNA clone IMAGE:2177857 3' Homo sapiens similar to SW:NU4M_PANTR P03906 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4.; mRNA sequence.	38,264	11-MAR-1999
rx01829	1446	GB_BA1:MLCB1770	37821	Z70722	Mycobacterium leprae cosmid B1770.	36,411	29-Aug-97
		GB_HTG2:AC008073	173144	AC008073	Homo sapiens clone NH0507M03, *** SEQUENCING IN PROGRESS ***; 3 Homo sapiens unordered pieces.	36,310	17-Jul-99
		GB_HTG2:AC008073	173144	AC008073	Homo sapiens clone NH0507M03, *** SEQUENCING IN PROGRESS ***; 3 Homo sapiens unordered pieces.	36,310	17-Jul-99
rx01868	2049	GB_IN1:AB018544	620	AB018544	Hydra magnipapillata mRNA for Hym-176 preprohormone, complete cds.	34,855	6-Feb-99
		GB_EST8:AA003136	450	AA003136	mg51e01.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone IMAGE:427320 5' similar to gb:X07315 PLACENTAL PROTEIN 15 (HUMAN);, mRNA sequence.	42,202	19-Jul-96
		GB_IN1:AB018544	620	AB018544	Hydra magnipapillata mRNA for Hym-176 preprohormone, complete cds.	35,968	6-Feb-99
rx01934	681	GB_BA1:MTV033	21620	AL021928	Mycobacterium tuberculosis H37Rv complete genome; segment 11/162.	38,679	17-Jun-98
		GB_BA1:MLCL622	42498	Z95398	Mycobacterium leprae cosmid L622.	38,911	24-Jun-97
		GB_BA1:MSG8983CS	36788	L78828	Mycobacterium leprae cosmid B983 DNA sequence.	38,933	15-Jun-96
rx01967	1266	GB_PR4:DJ534K4	216387	AF109907	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds; and S171 gene, partial cds.	39,189	23-DEC-1998
		GB_HTG2:AC006342	201618	AC006342	Homo sapiens clone DJ0054D12, *** SEQUENCING IN PROGRESS ***; 3 Homo sapiens unordered pieces.	34,412	11-Jan-99
		GB_HTG2:AC006342	201618	AC006342	Homo sapiens clone DJ0054D12, *** SEQUENCING IN PROGRESS ***; 3 Homo sapiens unordered pieces.	34,412	11-Jan-99
rx01993	1166	GB_IN2:AC005467	62091	AC005467	Drosophila melanogaster, chromosome 2R,-region 48C1-48C2, P1 clone DS00568, complete sequence.	35,252	12-DEC-1998
		GB_BA2:AE001678	13485	AE001678	Chlamydia pneumoniae section 94 of 103 of the complete genome.	35,203	08-MAR-1999
		GB_IN2:AC005467	62091	AC005467	Drosophila melanogaster, chromosome 2R, region 48C1-48C2, P1 clone DS00568, complete sequence.	34,699	12-DEC-1998
rx01994	1098	GB_BA1:PPVANAB	2864	Y14759	Pseudomonas putida vanA and vanB genes.	51,697	09-MAY-1998
		GB_HTG2:AC006799	278007	AC006799	Caenorhabditis elegans clone Y51H7, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	38,455	23-Feb-99
		GB_HTG2:AC006799	278007	AC006799	Caenorhabditis elegans clone Y51H7, *** SEQUENCING IN PROGRESS ***; 7 unordered pieces.	38,455	23-Feb-99
rx01997	609	GB_HTG4:AC009961	231522	AC009961	Homo sapiens chromosome unknown clone NH0357L02, WORKING DRAFT SEQUENCE, in unordered pieces.	35,576	29-OCT-1999
		GB_HTG4:AC009961	231522	AC009961	Homo sapiens chromosome unknown clone NH0357L02, WORKING DRAFT SEQUENCE, in unordered pieces.	35,576	29-OCT-1999
		GB_HTG4:AC009961	231522	AC009961	Homo sapiens chromosome unknown clone NH0357L02, WORKING DRAFT SEQUENCE, in unordered pieces.	35,472	29-OCT-1999
rx01999	299	GB_BA2:AF112536	1798	AF112536	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds.	37,719	5-Aug-99
		GB_BA1:SCH66	9153	AL049731	Streptomyces coelicolor cosmid H66.	38,655	29-Apr-99
		GB_EST29:AI558691	598	AI558691	fb79c10.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW:ATF3_HUMAN P18847 CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-3.; mRNA sequence.	40,232	24-MAR-1999

TABLE 4: ALIGNMENT RESULTS

rx02052	915	GB_EST3:R64206	453	R64206	yi18d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139599 5', mRNA sequence.	Homo sapiens	35,920	26-MAY-1995
		GB_PR2:AC002540	70851	AC002540	Human BAC clone GS025M02 from 7q21-q22, complete sequence.	Homo sapiens	37,099	12-Sep-97
		GB_GSS3:B55001	406	B55001	CIT-HSP-385H2.TRB CIT-HSP Homo sapiens genomic clone 385H2, genomic survey sequence.	Homo sapiens	35,599	20-Jun-98
rx02064	762	GB_PR4:AF135187	33016	AF135187	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds.	Homo sapiens	32,935	8-Jul-99
		GB_PR3:AC005612	60904	AC005612	Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence.	Homo sapiens	32,935	4-Sep-98
rx02082	3010	GB_PR1:HUM8DC11Z	3949	L35666	Homo sapiens (subclone H8 10_f11 from P1 35 H5 C8) DNA sequence.	Homo sapiens	31,995	22-Aug-94
		GB_BA1:MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	50,604	15-Jun-96
		GB_BA1:MTCY338	29372	Z74697	Mycobacterium tuberculosis H37Rv complete genome, segment 127/162.	Mycobacterium tuberculosis	38,113	17-Jun-98
		GB_GSS10:AQ242118	766	AQ242118	3123-4r Ochrobactrum anthropi BAC Library Ochrobactrum anthropi genomic clone 3123-4r, genomic survey sequence.	Ochrobactrum anthropi	41,876	02-OCT-1998
rx02083	1533	GB_PR4:AC008055	196899	AC008055	Homo sapiens 12q22-103.4-106.5 BAC RPC111-718L23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	36,818	09-OCT-1999
		GB_PL2:AC002292	120787	AC002292	Genomic sequence of Arabidopsis BAC F8A5, complete sequence.	Arabidopsis thaliana	37,517	02-OCT-1997
		GB_PR4:AC008055	196899	AC008055	Homo sapiens 12q22-103.4-106.5 BAC RPC111-718L23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,563	09-OCT-1999
rx02092	1761	GB_BA2:AF031929	2675	AF031929	Lactobacillus helveticus co-chaperonin GroES and chaperonin GroEL genes, complete cds; and DNA mismatch repair enzyme (hexA) gene, partial cds.	Lactobacillus helveticus	36,149	8-Aug-98
		GB_HTG1:HSDJ34F7	129811	AL049547	Homo sapiens chromosome 6 clone RP1-34F7, *** SEQUENCING IN PROGRESS ***. in unordered pieces.	Homo sapiens	37,587	23-Nov-99
rx02098	1869	GB_PR2:HSU24578	17488	U24578	Human RP1 and complement C4B precursor (C4B) genes, partial cds.	Homo sapiens	36,755	16-MAY-1996
		GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial ftsY and srp genes.	Corynebacterium glutamicum	99,766	14-MAY-1999
		GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial ftsY and srp genes.	Corynebacterium glutamicum	36,983	14-MAY-1999
rx02105	391	GB_EST17:AA660065	352	AA660065	EST00115 watermelon lambda zap express library Citrullus lanatus cDNA clone WMLS233 5' similar to translation initiation factor, mRNA sequence.	Citrullus lanatus	37,231	10-Nov-97
		GB_GSS6:AQ839377	523	AQ839377	HS_4640_B2_F09_T7A CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=4640 Col=18 Row=L, genomic survey sequence.	Homo sapiens	37,500	30-Aug-99
		GB_PL1:SPCC970	31438	AL031530	S.pombe chromosome III cosmid c970.	Schizosaccharomyces pombe	38,268	07-MAY-1999
rx02111	1407	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	50,791	24-MAR-1999
		GB_BA1:U00010	41171	U00010	Mycobacterium leprae cosmid B1170.	Mycobacterium leprae	37,563	01-MAR-1994
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome, segment 70/162.	Mycobacterium tuberculosis	39,504	24-Jun-99
rx02118	465	GB_HTG2:AC007164	158320	AC007164	Homo sapiens clone NH0304A10, *** SEQUENCING IN PROGRESS ***. 3 unordered pieces.	Homo sapiens	38,377	23-Apr-99
		GB_PR3:AC004451	108642	AC004451	Homo sapiens PAC clone DJ0789N01 from 7q21, complete sequence.	Homo sapiens	39,387	20-MAR-1998
		GB_HTG2:AC007164	158320	AC007164	Homo sapiens clone NH0304A10, *** SEQUENCING IN PROGRESS ***. 3 unordered pieces.	Homo sapiens	38,377	23-Apr-99

TABLE 4: ALIGNMENT RESULTS

rx02120	885	GB_PL2:PUMCDCZA	1288	L34206	Petroselinum crispum protein kinase p34cdc2 (cdc2) mRNA, complete cds.	Petroselinum crispum	37,816	17-Feb-96
		GB_GSS10:AQ214799	431	AQ214799	HS_3010_A2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=24 Row=M, genomic survey sequence.	Homo sapiens	34,591	18-Sep-98
		GB_PL2:PUMCDCZA	1288	L34206	Petroselinum crispum protein kinase p34cdc2 (cdc2) mRNA, complete cds.	Petroselinum crispum	36,541	17-Feb-96
rx02126	444	GB_GSS4:AQ0707596	485	AQ0707596	HS_5560_B1_H08_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1136 Col=15 Row=P, genomic survey sequence.	Homo sapiens	38,482	7-Jul-99
		GB_GSS13:AQ494885	411	AQ494885	HS_5195_A1_B11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=771 Col=21 Row=C, genomic survey sequence.	Homo sapiens	40,897	28-Apr-99
		GB_GSS4:AQ0707596	485	AQ0707596	HS_5560_B1_H08_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1136 Col=15 Row=P, genomic survey sequence.	Homo sapiens	43,533	7-Jul-99
rx02148	1266	GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING Homo sapiens IN PROGRESS ***, 33 unordered pieces.	Homo sapiens	36,051	24-Jun-99
		GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING Homo sapiens IN PROGRESS ***, 33 unordered pieces.	Homo sapiens	36,051	24-Jun-99
		GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING Homo sapiens IN PROGRESS ***, 33 unordered pieces.	Homo sapiens	35,402	24-Jun-99
rx02214	732	GB_GSS13:AQ459868	402	AQ459868	HS_5116_A1_H04_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=692 Col=7 Row=O, genomic survey sequence.	Homo sapiens	43,035	23-Apr-99
		GB_EST26:AU005050	790	AU005050	Bombyx mori p50(Daizo) Bombyx mori cDNA clone ws30188, mRNA sequence.	Bombyx mori	45,902	19-Jan-99
		GB_PL2:F8K7	98581	AC007727	Arabidopsis thaliana chromosome 1 BAC F8K7 sequence, complete sequence.	Arabidopsis thaliana	37,155	29-Jun-99
rx02316	1137	GB_EST32:AI723424	600	AI723424	hcgIs49.T7 Haemonchus contortus Intestinal mRNA Haemonchus contortus cDNA clone hcgIs49.T7 T7, mRNA sequence.	Haemonchus contortus	35,953	10-Jun-99
		GB_PR4:AC000134	203300	AC000134	Homo sapiens Chromosome 11q13 BAC Clone 137c7, complete sequence.	Homo sapiens	37,030	06-MAY-1999
		GB_STS:AF021124	575	AF021124	Homo sapiens trinucleotide repeat ctg-68, sequence tagged site.	Homo sapiens	41,913	3-Apr-98
rx02384	831	GB_PL1:ATA224957	4081	AJ224957	Arabidopsis thaliana RGAL gene.	Arabidopsis thaliana	35,627	19-MAY-1998
		GB_RO:AF022770	577	AF022770	Mus musculus peripheral benzodiazepine receptor associated protein (Pap7) mRNA, partial cds.	Mus musculus	39,652	24-Sep-97
		GB_GSS11:AQ258908	890	AQ258908	nbxb0021F23r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0021F23r, genomic survey sequence.	Oryza sativa	39,515	23-OCT-1998
rx02411	972	GB_BA1:AB020624	1605	AB020624	Corynebacterium glutamicum murI gene for D-glutamate racemase, complete cds.	Corynebacterium glutamicum	98,868	24-Jul-99
		GB_EST18:AA733776	385	AA733776	vv03f03.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1210589 5', mRNA sequence.	Mus musculus	43,864	7-Jan-98
		GB_EST38:AW033449	612	AW033449	EST277020 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC28F5, mRNA sequence.	Lycopersicon esculentum	35,620	15-Sep-99

TABLE 4: ALIGNMENT RESULTS

rx02448	1212	GB_BA1:AB016258	2260	AB016258	Arthrobacter sp. gene for maleylacetate reductase and hydroxyquinol 1,2-dioxygenase, partial and complete cds.	Arthrobacter sp.	60,465	8-Sep-99
		GB_EST37:AW014148	553	AW014148	UI-H-B10-aaj-c-04-0-UI.s1 NCL_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709487 3', mRNA sequence.	Homo sapiens	44,560	10-Sep-99
		GB_EST14:AA432042	543	AA432042	zw80f01.r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:782521 5' similar to WP:T12A7.1 CE06433 ; mRNA sequence.	Homo sapiens	36,522	22-MAY-1997
rx02449	1026	GB_BA1:AB016258	2260	AB016258	Arthrobacter sp. gene for maleylacetate reductase and hydroxyquinol 1,2-dioxygenase, partial and complete cds.	Arthrobacter sp.	66,244	8-Sep-99
		GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	39,899	8-Sep-97
		GB_BA1:AB016258	2260	AB016258	Arthrobacter sp. gene for maleylacetate reductase and hydroxyquinol 1,2-dioxygenase, partial and complete cds.	Arthrobacter sp.	70,410	8-Sep-99
rx02497	1050	GB_BA2:CGU31224	422	U31224	Corynebacterium glutamicum (ppx) gene, partial cds.	Corynebacterium glutamicum	96,445	2-Aug-96
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162.	Mycobacterium tuberculosis	59,429	17-Jun-98
		GB_BA1:SCE7	16911	AL049819	Streptomyces coelicolor cosmid E7.	Streptomyces coelicolor	39,510	10-MAY-1999
rx02526	1329	GB_GSS10:AQ240233	483	AQ240233	CIT-HSP-2385F9.TR.1 CIT-HSP Homo sapiens genomic clone 2385F9, genomic survey sequence.	Homo sapiens	42,475	30-Sep-98
		GB_OV:S48556	195	S48556	{tandem repeat P1 monomer} [Cacatua galerita=sulfur-crested cockatoo, Genomic, 195 nt].	Cacatua galerita	50,515	08-MAY-1993
		GB_PR2:HSM801056	2555	AL117532	Homo sapiens mRNA; cDNA DKFp434E192 (from clone DKFp434E192).	Homo sapiens	39,116	15-Sep-99
rx02530	780	GB_PR3:HSJ753D10	97912	AL049651	Human DNA sequence from clone 753D10 on chromosome 20 Contains genes for SSTR4(somatostatin receptor 4) and THBD(thrombomodulin), ESTs, STSs, GSSs and CpG islands, complete sequence.	Homo sapiens	34,248	23-Nov-99
		GB_EST33:AI782764	661	AI782764	EST263643 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES20B10, mRNA sequence.	Lycopersicon esculentum	35,385	29-Jun-99
		GB_GSS9:AQ121479	521	AQ121479	HS_3084_A2_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=4 Row=C, genomic survey sequence.	Homo sapiens	38,689	22-Sep-98
rx02535	1278	GB_HTG3:AC008710	146065	AC008710	Homo sapiens chromosome 5 clone CIT978SKB_7E3, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.	Homo sapiens	35,799	3-Aug-99
		GB_HTG3:AC008710	146065	AC008710	Homo sapiens chromosome 5 clone CIT978SKB_7E3, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.	Homo sapiens	35,799	3-Aug-99
		GB_HTG3:AC008710	146065	AC008710	Homo sapiens chromosome 5 clone CIT978SKB_7E3, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.	Homo sapiens	34,886	3-Aug-99
rx02603	1119	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162.	Mycobacterium tuberculosis	37,975	24-Jun-99
		GB_IN2:AC005714	177740	AC005714	Drosophila melanogaster, chromosome 2R, region 58D4-58E2, BAC clone BACR48M13, complete sequence.	Drosophila melanogaster	41,226	01-MAY-1999
		GB_EST19:AA775050	218	AA775050	ac76e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE:868554 3' similar to gb:Y00371_ma1 HEAT SHOCK COGNATE 71 KD PROTEIN (HUMAN); mRNA sequence.	Homo sapiens	40,826	5-Feb-98

rx02641

TABLE 4: ALIGNMENT RESULTS

rx02651	1053	GB_BA1:MTCY48 GB_BA1:SC4A10	35377 43147	Z74020 AL109663	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162. Streptomyces coelicolor cosmid 4A10.	Mycobacterium tuberculosis Streptomyces coelicolor A3(2)	62,678 39,109	17-Jun-98 5-Aug-99
rx02674	1575	GB_BA1:MLCL458 GB_BA2:PPU96338	43839 5276	AL049478 U96338	Mycobacterium leprae cosmid L458. Pseudomonas putida NCIMB 9866 plasmid pRA4000 p-cresol degradative pathway genes, p-hydroxybenzaldehyde dehydrogenase (pchA), p-cresol methylhydroxylase, cytochrome subunit precursor (pchC), unknown (pchX) and p-cresol methylhydroxylase, flavoprotein subunit (pchF) genes, complete cds.	Mycobacterium leprae Pseudomonas putida	62,753 58,095	27-Aug-99 13-MAY-1999
		GB_BA1:SCE9 GB_BA2:PPU96339	37730 4464	AL049841 U96339	Streptomyces coelicolor cosmid E9. Pseudomonas putida NCIMB 9869 plasmid pRA500 p-cresol degradative pathway genes, p-hydroxybenzaldehyde dehydrogenase (pchA) gene, partial cds, and p-cresol methylhydroxylase, cytochrome subunit (pchC), unknown (pchX), p-cresol methylhydroxylase, flavoprotein subunit (pchF), protocatechuate-3,4-dioxygenase, beta subunit (pcaH) and protocatechuate-3,4-dioxygenase, alpha subunit (pcaG) genes, complete cds.	Streptomyces coelicolor Pseudomonas putida	38,544 70,588	19-MAY-1999 13-MAY-1999
rx02702	1581	GB_BA1:AB015023	2291	AB015023	Corynebacterium glutamicum genes for MurC and FtsQ, complete cds.	Corynebacterium glutamicum	99,365	6-Feb-99
		GB_BA1:AB003132	4116	AB003132	Corynebacterium glutamicum gene for MurC, FtsQ, FtsZ, complete cds.	Corynebacterium glutamicum	99,317	4-Aug-97
		GB_BA1:BLFTSZ	5546	Y08964	B.lactofermentum murC, ftsQ or divD & ftsZ genes.	Corynebacterium glutamicum	99,296	08-OCT-1998
rx02703	1212	GB_BA1:AB015023	2291	AB015023	Corynebacterium glutamicum genes for MurC and FtsQ, complete cds.	Corynebacterium glutamicum	97,468	6-Feb-99
		GB_PL2:VFAMACTRA GB_PAT:E05047	1879 966	Y09591 E05047	V.faba mRNA for amino acid transporter. DNA encoding recombinant monoglyceride lipase.	Vicia faba Bacillus sp.	38,915 37,158	02-DEC-1999 29-Sep-97
rx02704	1812	GB_BA1:MTCY270 GB_BA2:AE000961	37586 18765	Z95388 AE000961	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162. Archaeoglobus fulgidus section 146 of 172 of the complete genome.	Mycobacterium tuberculosis Archaeoglobus fulgidus	37,946 38,521	10-Feb-99 15-DEC-1997
rx02705	1539	GB_BA1:MTCY270 GB_PAT:I26124 EM_PAT:E11760	37586 6911 6911	Z95388 I26124 E11760	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162. Sequence 4 from patent US 5556776. Base sequence of sucrase gene.	Mycobacterium tuberculosis Unknown. Corynebacterium glutamicum	37,850 97,619 97,619	10-Feb-99 07-OCT-1996 08-OCT-1997 (Rel. 52, Created)
rx02706	1221	GB_BA1:SC4A10 GB_PAT:I26124 EM_PAT:E11760	43147 6911 6911	AL109663 I26124 E11760	Streptomyces coelicolor cosmid 4A10. Sequence 4 from patent US 5556776. Base sequence of sucrase gene.	Streptomyces coelicolor A3(2) Unknown. Corynebacterium glutamicum	37,856 98,605 98,605	5-Aug-99 07-OCT-1996 08-OCT-1997 (Rel. 52, Created)
rx02707	1653	GB_BA1:MTCY270 EM_PAT:E11760	37586 6911	Z95388 E11760	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162. Base sequence of sucrase gene.	Mycobacterium tuberculosis Corynebacterium glutamicum	34,868 98,547	10-Feb-99 08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	98,547	07-OCT-1996

TABLE 4: ALIGNMENT RESULTS

rx02710	1686	GB_BA1:MLCB268 EM_PAT:E11760	38859 6911	AL022602 E11760	Mycobacterium leprae cosmid B268. Base sequence of sucrose gene.	Mycobacterium leprae Corynebacterium glutamicum	37,815 52,124	27-Aug-99 08-OCT-1997 (Rel. 52, Created) 07-OCT-1996 24-Apr-99
rx02711	2235	GB_PAT:I26124 GB_GSS13:AQ484169	6911 515	I26124 AQ484169	Sequence 4 from patent US 5556776. RPCI-11-264A12.TV RPCI-11 Homo sapiens genomic clone RPCI-11-264A12, genomic survey sequence.	Unknown. Homo sapiens	52,124 40,856	
		GB_BA2:XCU45994	1203	U45994	Xanthomonas campestris pv. campestris insertion sequence IS1404.	Xanthomonas campestris pv. campestris	39,061	29-Jan-99
		GB_BA2:XCU77781	4160	U77781	Xanthomonas campestris pv. amaranthicola XamI DNA methyltransferase (xamIM) gene, complete cds; insertion sequence IS1389 and unknown genes.	Xanthomonas campestris pv. 39,551 amaranthicola		9-Feb-99
rx02713	1134	GB_BA2:AF108355	1222	AF108355	Xanthomonas campestris pv. amaranthicola insertion sequence IS1389-B unknown genes.	Xanthomonas campestris pv. 40,281 amaranthicola		09-MAR-1999
		GB_BA1:MTCY270 GB_PR1:D31907	37586 599	Z95388 D31907	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162. Homo sapiens gene for zinc regulatory factor, partial cds.	Mycobacterium tuberculosis Homo sapiens	38,669 36,396	10-Feb-99 7-Feb-99
rx02716	684	GB_PR1:HSMTFMR GB_PR3:AC002347 GB_PR3:HS310J6	3302 134977 87942	X78710 AC002347 AL035593	H.sapiens MTF-1 mRNA for metal-regulatory transcription factor. Homo sapiens chromosome 17, clone 297N7, complete sequence. Human DNA sequence from clone 310J6 on chromosome 6q22.1-22.3. Contains part of a novel gene, ESTs, STSs and GSSs, complete sequence.	Homo sapiens Homo sapiens Homo sapiens	37,243 36,282 37,291	1-Aug-94 3-Feb-98 23-Nov-99
rx02722	1449	GB_HTG3:AC011509	111353	AC011509	Homo sapiens chromosome 19 clone CITB-H1_2189E23, *** SEQUENCING IN PROGRESS ***; 35 unordered pieces.	Homo sapiens	37,407	07-OCT-1999
		GB_BA1:BLFTSZ	5546	Y08964	B.lactofermentum murC, ftsQ or divD & ftsZ genes.	Corynebacterium glutamicum	99,652	08-OCT-1998
		GB_BA1:AB003132	4116	AB003132	Corynebacterium glutamicum gene for MurC, FtsQ, FtsZ, complete cds.	Corynebacterium glutamicum	98,535	4-Aug-97
		GB_PAT:E17182	1125	E17182	Brevibacterium flavum ftsQ gene complete cds.	Corynebacterium glutamicum	97,235	28-Jul-99
rx02723	789	GB_BA1:AB015023	2291	AB015023	Corynebacterium glutamicum genes for MurC and FtsQ, complete cds.	Corynebacterium glutamicum	99,113	6-Feb-99
		GB_BA1:BLFTSZ	5546	Y08964	B.lactofermentum murC, ftsQ or divD & ftsZ genes.	Corynebacterium glutamicum	99,113	08-OCT-1998
		GB_BA1:AB003132	4116	AB003132	Corynebacterium glutamicum gene for MurC, FtsQ, FtsZ, complete cds.	Corynebacterium glutamicum	99,113	4-Aug-97
rx02813	1108	GB_HTG3:AC009658	171795	AC009658	Homo sapiens chromosome 15 clone 344_A_16 map 15, *** SEQUENCING IN PROGRESS ***; 29 unordered pieces.	Homo sapiens	34,622	01-OCT-1999
		GB_HTG3:AC009658	171795	AC009658	Homo sapiens chromosome 15 clone 344_A_16 map 15, *** SEQUENCING IN PROGRESS ***; 29 unordered pieces.	Homo sapiens	34,622	01-OCT-1999
rx02820	1411	GB_RO:MMU65079 GB_BA1:BFU64514	2300 3837	U65079 U64514	Mus musculus actin-binding protein (ENC-1) mRNA, complete cds. Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds.	Mus musculus Bacillus firmus	35,013 36,859	29-Jul-97 1-Feb-97
		GB_IN1:CET04C10	20958	Z69885	Caenorhabditis elegans cosmid T04C10, complete sequence.	Caenorhabditis elegans	35,934	2-Sep-99

TABLE 4: ALIGNMENT RESULTS

GB_EST35:AI823090	720	AI823090	L30-944T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-944 5' similar to 60S ribosomal protein L36 (AC004684)[Arabidopsis thaliana], mRNA sequence.	Mesembryanthemum crystallinum	35,770	21-Jul-99
rx02828 572						
GB_BA1:MTCY10H4	39160	Z80233	Mycobacterium tuberculosis H37Rv complete genome; segment 2/162.	Mycobacterium tuberculosis	39,823	17-Jun-98
GB_BA1:MTORIREP	8400	X92504	M.tuberculosis origin of replication and genes rnpA, rpmH, dnaA, dnaN, recF.	Mycobacterium tuberculosis	39,823	26-Aug-97
GB_RO:RATENDOGLY	3906	L37380	Rat apical endosomal glycoprotein mRNA, complete cds.	Rattus norvegicus	38,704	20-Apr-95
GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	99,362	17-DEC-1993
GB_BA2:AE000477	11314	AE000477	Escherichia coli K-12 MG1655 section 367 of 400 of the complete genome.	Escherichia coli	99,787	12-Nov-98
rx02839 470						
GB_BA1:ECOPLSB	3865	K00127	E.coli plsB and dgk genes coding for sn-glycerol-3-phosphate acyltransferase and diglyceride kinase.	Escherichia coli	33,761	28-Feb-94
rx03218						